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Attorney Docket No.: 10203.204-US

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Svendsen et al.

Confirmation No: 3589

Serial No.: 10/786,850

Group Art Unit: 1646

Filed: February 24, 2004

~~Examiner:~~ TBA

For: Novel Subtilases

TRANSMITTAL OF CERTIFIED COPY OF PRIORITY APPLICATION(S)

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Sir:

Attached please find a certified copy of the foreign application from which priority is claimed for this case:

Country: DK
Application Number: PA 2003 00689
Filing Date: May 7, 2003

Country: DK
Application Number: PA 2003 00119
Filing Date: January 30, 2003

Respectfully submitted,

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Date: July 2, 2004



Kongeriget Danmark

Patent application No.: PA 2003 00689
Date of filing: 07 May 2003
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Title: Novel subtilases

IPC: -

This is to certify that the attached documents are exact copies of the above mentioned patent application as originally filed.



Patent- og Varemærkestyrelsen
Økonomi- og Erhvervsministeriet

18 June 2004

Pia Høybye-Olsen

7 MAJ 2003

NOVEL SUBTILASES

PVS

FIELD OF THE INVENTION

The present invention relates to variants of TY145 subtilases and BPN' subtilases and to
5 methods of construction such variants with altered properties, such as stability (e.g. ther-
mostability or storage stability), Ca^{2+} dependency, pH dependent activity.

BACKGROUND OF THE INVENTION

Enzymes have been used within the detergent industry as part of washing formulations for
10 more than 30 years. Proteases are from a commercial perspective the most relevant en-
zyme in such formulations, but other enzymes including lipases, amylases, cellulases,
hemicellulases or mixtures of enzymes are also often used.

To improve the cost and/or the performance of proteases there is an ongoing search for
proteases with altered properties, such as increased activity at low temperatures, increased
15 thermostability, increased specific activity at a given pH, altered Ca^{2+} dependency, in-
creased stability in the presence of other detergent ingredients (e.g. bleach, surfactants
etc.) etc.

The search for proteases with altered properties include both discovery of naturally occur-
ring proteases, i.e. so called wild-type proteases but also alteration of well-known prote-
ases by e.g. genetic manipulation of the nucleic acid sequence encoding said proteases.
20 Knowledge of the relationship between the three-dimensional structure and the function of
a protein has improved the ability to evaluate which areas of a protein to alter to affect a
specific characteristic of the protein.

One family of proteases, which are often used in detergents, are the subtilases. This family
25 has previously been further grouped into 6 different sub-groups by Siezen RJ and Leunis-
sen JAM, 1997, Protein Science, 6, 501-523. One of these sub-groups is the Subtilisin fam-
ily which includes subtilases such as BPN', subtilisin 309 (SAVINASE[®], NOVOZYMES
A/S), subtilisin Carlsberg (ALCALASE[®], NOVOZYMES A/S), subtilisin S41 (a subtilase
from the psychrophilic Antarctic *Bacillus* TA41, Davail S et al. 1994, The Journal of Biologi-
30 cal Chemistry, 269(26), 99. 17448-17453), subtilisin S39 (a subtilase from the psychrophilic
Antarctic *Bacillus* TA39, Narinx E et al. 1997, Protein Engineering, 10 (11), pp. 1271-1279)
and TY145 (a subtilase from *Bacillus* sp. TY145, NCIMB 40339 described in WO
92/17577).

However, despite the sequence homology between the subtilases belonging to the Subtil-
35 isin subgroup of subtilases, modelling of the three-dimensional structure of one subtilase

on the basis of the three-dimensional structure of another subtilase may result in an incorrect three-dimensional structure because of structural differences.

The inventors of the present invention have elucidated the three-dimensional structure of the TY145 subtilase and found that there are several differences between this and the three-dimensional structure of BPN' also belonging to the Subtilisin subgroup of subtilases. This surprising difference in structure makes it advantageous to use the TY145 structure as basis for homology modelling of TY145 like subtilisins, which, in turn, will improve the ability to obtain desired changes in functionality by protein engineering.

Two studies have used protein engineering to alter functionality of TY145 like subtilisins: Miyazaki K et al. 2000, J Mol Biol, 297, pp.1015-1026 discloses enhancement of the thermostability and activity of the psychrophilic protease subtilisin S41 by methods of directed evolution.

Wintrode TL et al. 2000, Journal of Biological Chemistry, 275 (41), pp.31635-31640 discloses conversion of a mesophilic subtilisin-like protease from *Bacillus sphaericus* SSII into its psychrophilic counterpart by methods of directed evolution. Wintrode et al. constructed the three-dimensional structural model of the SSII subtilase on basis of its homology with subtilisins Carlsberg, Savinase, BPN' and Thermitase. However, according to the present invention the SSII subtilase pertain to the new group of TY145 like subtilases and thus the modelling of SSII based on the 3D structure of the BPN' like subtilases will likely give an inaccurate result.

The differences between the three-dimensional structures of TY145 and BPN' are confirmed by the recently published three-dimensional structure of the subtilase "sphericase" from *Bacillus sphaericus* (PDB NO:1EA7, Protein Data Bank). The overall structure and many details of this subtilase are very homologous with the TY145 subtilase structure.

BRIEF DESCRIPTION OF THE INVENTION

The inventors have modified the amino acid sequence of a subtilase to obtain variants with improved properties, based on the three-dimensional structure of the subtilases TY145 and BPN'. The variants have altered properties, such as increased activity at low temperatures, increased thermostability, increased specific activity at a given pH, altered Ca^{2+} dependency, increased stability in the presence of other detergent ingredients (e.g. bleach, surfactants etc.) etc.

Accordingly, the object of the present invention is to provide a method for constructing subtilases having altered properties, in particular to provide a method for constructing subtilases having altered properties as described above.

Thus, in its broadest aspect, the present invention relates to a method for constructing a variant of a parent subtilase, wherein the variant has at least one altered property as compared to said parent subtilase, which method comprises:

- 5 i) analyzing the three-dimensional structure of the subtilase to identify, on the basis of an evaluation of structural considerations, at least one amino acid residue or at least one structural region of the subtilase, which is of relevance for altering said property;
- ii) constructing a variant of the subtilase, which as compared to the parent subtilase, has been modified in the amino acid residue or structural part identified in i) so as to alter said property; and
- 10 iii) testing the resulting subtilase variant for said property.

Although it has been described in the following that modification of the parent subtilase in certain regions and/or positions is expected to confer a particular effect to the thus produced subtilase variant, it should be noted that modification of the parent subtilase in any of
 15 such regions may also give rise to any other of the above-mentioned effects. For example, any of the regions and/or positions mentioned as being of particular interest with respect to, e.g., improved thermostability, may also give rise to, e.g., higher activity at a lower pH, an altered pH optimum, or increased specific activity, such as increased peptidase activity.

Further aspects of the present invention relates to variants of a subtilase, the DNA encoding such variants and methods of preparing the variants. Still further aspects of the present
 20 invention relates to the use of the variants for various industrial purposes, in particular as an additive in detergent compositions. Other aspects of the present invention will be apparent from the below description as well as from the appended claims.

25 **BRIEF DESCRIPTION OF DRAWINGS**

Figure 1, Multiple alignment of 3D sequences of subtilases from TY145, TA39, TA41, *Bacillus sphaericus* and Savinase.

Figure 2, Matrix of homology between subtilases pertaining to the TY145 and BPN' sub-
 30 groups. The sequences are identified by sequence database accession numbers.

- 1: q45681; Subtilase derived from *B. subtilis* (BSTA41)
- 2: p28842; Psychrophilic subtilisin derived from Antarctic *Bacillus* strain (BSTA39)
- 3: abb77095; Subtilase derived from *Bacillus* sp. (TY145)
- 4: p00783; Subtilase derived from *Bacillus subtilis* var. *amylosacchariticus* (BSAMY)
- 35 5: p29142; Subtilase derived from *Bacillus stearothermophilus* (BSSJ)

- 6: p35835; Subtilase derived from *Bacillus subtilis* var. *natto*. (BSNAT)
- 7: p07518; Subtilase derived from *Bacillus pumilus* (*B. mesentericus*) (BPMES)
- 8: p00782; Subtilase derived from *Bacillus amyloliquefaciens* (BPN')
- 9: p00780; Subtilase derived from *Bacillus licheniformis* (BLSCAR)
- 5 10: p41363; Subtilase derived from *Bacillus halodurans* (BHSAH)
- 11: aaw62222; Subtilase derived from *Bacillus lentus* (BLS147)
- 12: p29600; Subtilase derived from *Bacillus lentus* (BLSAVI, BLS309)
- 13: p27693; Subtilase derived from *Bacillus alcalophilus* (BAALKP)
- 14: q99405; Subtilase derived from *Bacillus* sp. strain KSM-K16 (BSKSMK)
- 10 15: p29599; Subtilase derived from *Bacillus lentus* (BLSUBL).

Figure 3, Alignment of TY145 subtilase (blue/dark) and BPN' structures (red/light), with indication of ion-binding sites. TY145 sites are yellow (light) and BPN' sites are green (dark).

- 15 APPENDIX 1 shows the structural coordinates for the solved crystal 3D structure of the TY145 subtilase.

DEFINITIONS

- 20 Prior to discussing this invention in further detail, the following terms and conventions will first be defined.

For a detailed description of the nomenclature of amino acids and nucleic acids, we refer to WO 00/71691 page 5, hereby incorporated by reference. A description of the nomenclature of modifications introduced in a polypeptide by genetic manipulation can be found in WO 00/71691 page 7-12, hereby incorporated by reference.

- 25 The term "subtilases" refer to a sub-group of serine protease according to Siezen *et al.*, *Protein Engng.* 4 (1991) 719-737 and Siezen *et al.* *Protein Science* 6 (1997) 501-523. Serine proteases or serine peptidases is a subgroup of proteases characterised by having a serine in the active site, which forms a covalent adduct with the substrate. Further the subtilases (and the serine proteases) are characterised by having two active site amino acid residues apart from the serine, namely a histidine and an aspartic acid residue.
- 30

- Subtilases are defined by homology analysis of more than 170 amino acid sequences of serine proteases previously referred to as subtilisin-like proteases. The subtilases may be divided into 6 sub-divisions, i.e. the Subtilisin family, the Thermitase family, the Proteinase K family, the Lantibiotic peptidase family, the Kexin family and the Pyrolysin family.
- 35

The Subtilisin family (EC 3.4.21.62) may be further divided into 3 sub-groups, i.e. I-S1 ("true" subtilisins), I-S2 (highly alkaline proteases) and intracellular subtilisins. Definitions or grouping of enzymes may vary or change, however, in the context of the present invention the above division of subtilases into sub-division or sub-groups shall be understood as those described by Siezen et al., *Protein Engng.* 4 (1991) 719-737 and Siezen et al. *Protein Science* 6 (1997) 501-523.

The term "parent" is in the context of the present invention to be understood as a protein, which is modified to create a protein variant. The parent protein may be a naturally occurring (wild-type) polypeptide or it may be a variant thereof prepared by any suitable means. For instance, the parent protein may be a variant of a naturally occurring protein which has been modified by substitution, chemical modification, deletion or truncation of one or more amino acid residues, or by addition or insertion of one or more amino acid residues to the amino acid sequence, of a naturally-occurring polypeptide. Thus the term "parent subtilase" refers to a subtilase which is modified to create a subtilase variant.

The term "variant" is in the context of the present invention to be understood as a protein which has been modified as compared to a parent protein at one or more amino acid residues.

The term "modification(s)" or "modified" is in the context of the present invention to be understood as to include chemical modification of a protein as well as genetic manipulation of the DNA encoding a protein. The modification(s) may be replacement(s) of the amino acid side chain(s), substitution(s), deletion(s) and/or insertions in or at the amino acid(s) of interest. Thus the term "modified protein", e.g. "modified subtilase", is to be understood as a protein which contains modification(s) compared to a parent protein, e.g. subtilase.

The term "(a) TY145 subtilase" or "(a) TY145 like subtilase" should in the context of the present invention be understood as a subtilase belonging to the Subtilisin group according to Siezen et al. *Protein Science* 6 (1997) 501-523 and which has at least 63% homology to TY145 SEQ ID NO:1. In the context of the present invention a TY145 subtilase has three ion-binding sites.

The term "(a) BPN' subtilase" or "(a) BPN' like subtilase" should in the context of the present invention be understood as a subtilase belonging to the Subtilisin group according

Siezen et al. Siezen et al. *Protein Science* 6 (1997) 501-523 and which has at least 61% homology to BPN' SEQ ID NO:5. Such a BPN' like subtilase is for example Savinase. In the context of the present invention a BPN' subtilase has two, three or five ion-binding sites. A BPN' like subtilase may, in the context of the present invention, belong to branch I-S of the subtilisins i.e. to branch I-S1, the "true" subtilisins or I-S2, the highly alkaline proteases (Siezen et al., *Protein Engng.* 4 (1991) 719-737).

"Homology" or "homologous to" is in the context of the present invention to be understood in its conventional meaning and the "homology" between two amino acid sequences should be determined by use of the "Similarity" defined by the GAP program from the University of Wisconsin Genetics Computer Group (UWGCG) package using default settings for alignment parameters, comparison matrix, gap and gap extension penalties. Default values for GAP penalties, i.e. GAP creation penalty of 3.0 and GAP extension penalty of 0.1 (Program Manual for the Wisconsin Package, Version 8, August 1994, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711). The method is also described in S.B. Needleman and C.D. Wunsch, *Journal of Molecular Biology*, 48, 443-445 (1970). Identities can be extracted from the same calculation. The homology between two amino acid sequences can also be determined by "identity" or "similarity" using the GAP routine of the UWGCG package version 9.1 with default setting for alignment parameters, comparison matrix, gap and gap extension penalties can also be applied using the following parameters: gap creation penalty = 8 and gap extension penalty = 8 and all other parameters kept at their default values. The output from the routine is besides the amino acid alignment the calculation of the "Percent Identity" and the "Similarity" between the two sequences. The numbers calculated using UWGCG package version 9.1 is slightly different from the version 8.

The term "position" is in the context of the present invention to be understood as the number of an amino acid in a peptide or polypeptide when counting from the N-terminal end of said peptide/polypeptide. The position numbers used in the present invention refer to different subtilases depending on which subgroup the subtilase belongs to.

The four known subtilases belonging to the TY145 subgroup, i.e. subtilases obtained from TY145, TA39, TA41 and *Bacillus sphaericus* are numbered individually according to each of SEQ ID NO:1,2,3 and 4.

Likewise other subtilases belonging to the TY145 subgroup are numbered individually according to their own sequence. However in order to determine homologous positions in such other subtilases an alignment with the each of SEQ ID's NO:1,2,3 and 4 is conducted according to the GAP procedure described above. Subsequently the homologous positions are determined in with reference to the most homologous of SEQ ID's NO:1,2,3 and 4. Alternatively subtilases belonging to the TY145 subgroup can be numbered by reference to the positions of TY145 subtilase (SEQ ID NO:1).

Subtilases belonging to the BPN' subgroup refers to the positions of Subtilisin Novo (BPN') from *B. amyloliquefaciens* (SEQ ID NO:5).

DETAILED DESCRIPTION OF THE INVENTION

Despite the great homology of the subtilases described above the inventors of the present invention have elucidated the three-dimensional structure of TY145, SEQ ID NO:1 by X-ray crystallography and found that there are several differences between this and the three-dimensional structure of BPN'. The inventors of the present invention have further compared the sequence homology of subtilases belonging to the Subtilisin subgroup. This is shown in the homology matrix in Figure 2 of the present invention.

On the basis of the 3D structure comparison and protein sequence the inventors of the present invention find that the subgroup of TY145 subtilases are different from BPN' subtilases based on the 3D structure comparison of the enclosed 3D structure of TY145 and the BPN' 3D structure but also indicated from the sequence homology between TY145 and BPN'.

TY145 subtilases

As described above a TY145 subtilase is in the context of the present invention to be understood as a subtilase which has at least 63% homology to SEQ ID NO:1. In particular said TY145 subtilase may have at least 65%, such as at least 70%, at least 74%, at least 80%, at least 83%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% homology to TY145, i.e. to SEQ ID NO:1.

In a first embodiment of the present invention a TY145 subtilase suitable for the purpose described herein may be a subtilase homologous to the three-dimensional structure of

TY145, i.e. it may be homologous to the three-dimensional structure defined by the structure coordinates in Appendix 1.

As it is well-known to a person skilled in the art that a set of structure coordinates for a protein or a portion thereof is a relative set of points that define a shape in three dimensions, it is possible that an entirely different set of coordinates could define an identical or a similar shape. Moreover, slight variations in the individual coordinates may have little or no effect on the overall shape.

These variations in coordinates may be generated because of mathematical manipulations of the structure coordinates. For example, the structure coordinates of Appendix 1 (TY145 structure) may be manipulated by crystallographic permutations of the structure coordinates, fractionalization of the structure coordinates, integer additions or subtractions to sets of the structure coordinates, inversion of the structure coordinates or any combination of the above. Alternatively, said variations may be due to differences in the primary amino acid sequence.

If such variations are within an acceptable standard error as compared to the structure coordinates of Appendix 1 said three-dimensional structure is within the context of the present invention to be understood as being homologous to the structure of Appendix 1. The standard error may typically be measured as the root mean square deviation of e.g. conserved backbone residues, where the term "root mean square deviation" (RMS) means the square root of the arithmetic mean of the squares of the deviations from the mean.

As it is also well-known to a person skilled in the art that within a group of proteins which have a homologous structure there may be variations in the three-dimensional structure in certain areas or domains of the structure, e.g. loops, which are not or at least only of a small importance to the functional domains of the structure, but which may result in a big root mean square deviation of the conserved residue backbone atoms between said structures.

Thus it is well known that a set of structure coordinates is unique to the crystallised protein. No other three dimensional structure will have the exact same set of coordinates, be it a homologous structure or even the same protein crystallised in different manner. There are natural fluctuations in the coordinates. The overall structure and the inter-atomic relationship can be found to be similar. The similarity can be discussed in terms of root mean square deviation of each atom of a structure from each "homologous" atom of another structure. However, only identical proteins have the exact same number of atoms. There-

fore, proteins having a similarity below 100% will normally have a different number of atoms, and thus the root mean square deviation can not be calculated on all atoms, but only the ones that are considered "homologous". A precise description of the similarity based on the coordinates is thus difficult to describe and difficult to compute for homologous proteins.

Regarding the present invention, similarities in 3D structure of different subtilases can be described by the content of homologous structural elements, and/or the similarity in amino acid or DNA sequence. For sequences having no deletions or insertions a RMS for the calcium atoms can be calculated.

Examples of TY145 like subtilases include the psychrophilic subtilisin protease S41 derived from the Antarctic *Bacillus* TA41, herein also called TA41 subtilase (Davail S et al., 1994, J. Biol. Chem., 269, 17448-17453), and the psychrophilic subtilisin protease S39 derived from the Antarctic *Bacillus* TA39, herein also called TA39 subtilase (Narinx E et al., 1997, Protein Engineering, 10 (11), 1271-1279). Recently a three-dimensional structure of a subtilisin homologous with the TY145 subtilisins was published in the Protein Data Bank (Accession No:1EA7). The overall structure and many details of this *Bacillus sphaericus* "sphericase" subtilase are very homologous with the TY145 subtilase structure; however the structure of the sphericase revealed as much as five ion-binding sites. The number of ion-binding sites may vary in similar structures depending on the medium used for crystallisation. Thus it appears that the two extra ion-binding sites of *Bacillus sphaericus* "sphericase" are due to a calcium containing crystallisation medium.

Accordingly, a preferred embodiment of the present invention is a parent subtilase or a subtilase variant which is at least 63% homologous to the sequence of SEQ ID NO:1, preferably at least 65%, at least 70%, at least 74%, at least 80%, at least 83%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% homologous to the sequence of SEQ ID NO:1, and optionally said subtilase further comprises the following structural characteristics:

- a) a twisted beta-sheet with 7 strands,
- b) six alpha helices,
- c) at least three ion-binding sites and

wherein the Strong ion-binding site of the BPN' like subtilases is not present, and with the exception of the TY145 subtilase, the TA39 subtilase, the TA41 subtilase, and the *Bacillus sphaericus* "sphericase".

The TY145 subtilase of the present invention is encoded by an isolated nucleic acid sequence, which nucleic acid sequence has at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% homology with the nucleic acid sequence shown in SEQ ID NO:20.

Further the isolated nucleic acid sequence encoding a TY145 subtilase of the invention hybridizes with a complementary strand of the nucleic acid sequence shown in SEQ ID NO:20 preferably under low stringency conditions, at least under medium stringency conditions, at least under medium/high stringency conditions, at least under high stringency conditions, at least under very high stringency conditions.

Suitable experimental conditions for determining hybridization at *low, medium, or high stringency between a nucleotide probe and a homologous DNA or RNA sequence involves presoaking of the filter containing the DNA fragments or RNA to hybridize in 5 x SSC (Sodium chloride/Sodium citrate, Sambrook et al. 1989) for 10 min, and prehybridization of the filter in a solution of 5 x SSC, 5 x Denhardt's solution (Sambrook et al. 1989), 0.5 % SDS and 100 µg/ml of denatured sonicated salmon sperm DNA (Sambrook et al. 1989), followed by hybridization in the same solution containing a concentration of 10ng/ml of a random-primed (Feinberg, A. P. and Vogelstein, B. (1983) *Anal. Biochem.* 132:6-13), ³²P-dCTP-labeled (specific activity > 1 x 10⁹ cpm/µg) probe for 12 hours at ca. 45°C. The filter is then washed twice for 30 minutes in 2 x SSC, 0.5 % SDS at least * 55°C (low stringency), more preferably at least 60°C (medium stringency), still more preferably at least 65°C (medium/high stringency), even more preferably at least 70°C (high stringency), and even more preferably at least 75°C (very high stringency).

BPN' subtilases

As described above a BPN' subtilase is in the context of the present invention to be understood as a subtilase which has at least 61% homology to SEQ ID NO:5. In particular said BPN' subtilase may have at least 70%, such as at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% homology to BPN', i.e. to SEQ ID NO:5.

In one embodiment of the present invention a BPN' subtilase suitable for the purpose described herein may be a subtilase homologous to the three-dimensional structure of BPN'

as defined by the structure coordinates given in PDB Nos. 1SBT and 1GNS (Protein Data Bank), or one of the several other structures of BPN' that are accessible from the Protein Data Bank. Variations between homologous structures may occur for several reasons as described above. Thus a BPN' subtilase within the context of the present invention is to be understood as any subtilase having the structural characteristics pertaining to the BPN' subtilases as described above, and in addition such subtilases does preferably not have further structural characteristics which are not present in the BPN' subtilases as described herein. Further a BPN' subtilase of the present invention may have the necessary percentage of similarity with SEQ ID NO:5.

Examples of BPN' like subtilases include the subtilisin 309 (PDB NO:1SVN SAVINASE®, NOVOZYMES A/S) and subtilisin Carlsberg (ALCALASE®, NOVOZYMES A/S), among others.

In figure 1 of R.J. Siezen and J.A.M Leunissen (Protein science, Vol. 6 (3), pp. 501-523, 1997) page 502 a structure of subtilases is described. A subtilase consists of 6-8 helices, 11 strands of which 7 are central in a twisted beta-sheet. Two ion-binding sites are mentioned, one of which is the so called "Weak" calcium-binding site. It was later discovered that for some structures (subtilisin DY PDB no. 1BH6, 1998), this calcium-binding site was shown to be a Na (sodium) binding site when the calcium concentration in the crystallization medium was low. Thus, in the following we refer to ion-binding sites instead of calcium-binding sites.

The BPN' subtilase of the present invention is encoded by an isolated nucleic acid sequence, which nucleic acid sequence has at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% homology with the nucleic acid sequence shown in SEQ ID NO:21.

Further the isolated nucleic acid sequence encoding a BPN' subtilase of the invention hybridizes with a complementary strand of the nucleic acid sequence shown in SEQ ID NO:21 preferably under low stringency conditions, but at least under medium stringency conditions, at least under medium/high stringency conditions, at least under high stringency conditions, at least under very high stringency conditions.

Three-dimensional structure of TY145 subtilases

The TY145 subtilase was used to elucidate the three-dimensional structure forming the basis for the present invention.

The structure of TY145 was solved in accordance with the principle for x-ray crystallographic methods, for example, as given in X-Ray Structure Determination, Stout, G.K. and Jensen, L.H., John Wiley & Sons, Inc. NY, 1989.

The structural coordinates for the solved crystal structure of TY145 are given in standard PDB format (Protein Data Bank, Brookhaven National Laboratory, Brookhaven, CT) as set forth in Appendix 1. It is to be understood that Appendix 1 forms part of the present application. In the context of Appendix 1, the following abbreviations are used: CA refers to c-alpha (carbon atoms) or to calcium ions, (however to avoid misunderstandings we use the full names "c-alpha atoms" and "calcium" or "ion" in the present specification). Amino acid residues are given in their standard three-letter code. The attached structural coordinates contain the protease structure, and an inhibitor structure CI2 as well as water molecules. The protease coordinates has a chain identification called A, whereas the CI2 inhibitor is called B, the calcium ions are called C, and the water is W. In the following the positions of the mentioned residues refer to the sequence of TY145 as disclosed in SEQ ID NO:1.

The structure of TY145 shows the same "overall" fold as found in the S8 family of subtilisins. The structure comprises a twisted beta-sheet with 7 strands arranged in the following sequential order S2, S3, S1, S4, S5, S6, S7. There are six alpha helices in the structure of which number H1 contains residues 9-15, H2 contains residues 72-81, H3 contains residues 114-131, H4 contains residues 148-158, H5 contains residues 250-267 and H6 contains residues 273-286.

The TY145 like subtilases are shown to lack the well-known Strong ion-binding site of the BPN' subtilases. However, in addition to the Weak calcium or ion-binding site also known from the BPN' subtilases, the TY145 subtilases have two ion-binding sites which are not present in the BPN' subtilisin structures. This can be seen in the structural alignment presented in Figure 3. These additional ion-binding sites are hereinafter referred to as "Near" and "Far" according to their distance to the Weak ion-binding site. Thus in relation to the atomic coordinates disclosed in Appendix 1, the ion-binding sites of TY145 are located at:

Weak - calcium atom named C 314,

Near - calcium atom named C 312, and

Far - calcium atom named C 313 in the PDB table (Appendix 1).

The position of an ion-binding site can be defined by the distance to four specific atoms in the core structure. The distance from the ion-binding site to the c-alpha atoms of the three active site residues has been chosen. Throughout the subtilases the residues Ser, His and Asp in the active site are highly conserved. In TY145 they are Asp35, His72 and Ser251. The fourth distance chosen is the distance to the c-alpha atom of the amino acid residue coming first after the active site serine residue in the sequence (herein after called "next to Ser"); in the 3D structure of TY145 it is Met252.

In a preferred embodiment of the present invention, the distance between:

- a) the Weak ion-binding site and i) Asp c-alpha atom is 17.50-19.50Å, ii) His c-alpha atom is 21-23Å, iii) Ser c-alpha atom is 13.80-15.80Å, iv) next to Ser c-alpha atom is 15.80-17.80Å,
- b) the Far ion-binding site and i) Asp c-alpha atom is 28.70-30.70Å, ii) His c-alpha atom is 28-30Å, iii) Ser c-alpha atom is 20-22Å, iv) next to Ser c-alpha atom is 19.50-21.50Å,
- c) the Near ion-binding site and i) Asp c-alpha atom is 27-29Å, ii) His c-alpha atom is 29.50-31.50Å, iii) Ser c-alpha atom is 21.40-23.40Å, iv) next to Ser c-alpha atom is 22.50-24.50Å.

Below are the specific distances between the four chosen c-alpha atoms and the three ion binding sites of the TY145 subtilase given in Å:

	Weak ion-binding site	Far ion-binding site	Near ion-binding site
Met252 c-alpha atom	16.75	20.35	23.58
His72 c-alpha atom	21.98	29.10	30.43
Asp35 c-alpha atom	18.55	29.68	28.04
Ser251 c-alpha atom	14.71	20.96	22.28
Weak ion-binding site	0	16.62	9.79
Far ion-binding site	16.62	0	12.48
Near ion-binding site	9.79	12.48	0

However these distances may vary from one subtilase to the other, and as described above, the Weak ion binding site may also bind to a sodium ion. The present distances are given with a calcium ion in the structure. If a sodium ion was bound instead the distances would be shifted a little bit. Generally the distances can vary $\pm 0.8\text{\AA}$, preferably $\pm 0.7\text{\AA}$, $\pm 0.6\text{\AA}$, $\pm 0.5\text{\AA}$, $\pm 0.4\text{\AA}$, or most preferably $\pm 0.3\text{\AA}$.

Further, in the TY145 like subtilases, the peptide structure circumventing the Weak ion-binding site is composed of the amino acid residues placed in positions 182-189 and 221-

227 with the coordinating atoms being the backbone carbonyl oxygen atom of residues G182, A187, L184 and two water molecules.

The peptide structure circumventing the Near ion-binding site is composed of residues 212-225 with the coordinating atoms being the backbone carbonyl oxygen atom of residues I220 and T215, the oxygens from the carboxylic acids of residues D225 and D218 and the amid group of residue Q222.

The peptide structure circumventing the Far ion-binding site is composed of residues 288-306 with the coordinating atoms being the backbone carbonyl oxygen atom of residues G298, G296 and I289, the oxygens from the carboxylic acids of residues D300 and D288, and two water molecules.

In comparison with the BPN' like subtilase structures the structure of the TY145 like subtilase can be divided into a "common subtilase-like" region, an "intermediate" region and a "nonhomologous" region.

The active site can be found in the common subtilase-like region, which is structurally closely related to the BPN' structures. The common subtilase-like region is composed of residues 88-128 and 225-284, and contains the alpha-helix H3 and the central alpha-helix H5 in which the active site serine residue is situated in the N-terminal part. The common subtilase-like region has an RMS lower than 1.2.

Outside the common subtilase-like region the structure of the TY145 like subtilase differs from the BPN' structures to a greater extent.

The intermediate region consist of residues 24-45, 48-58, 65-66, 67-85, 134-174, 175-196, 202-212 and 287-290. The intermediate region has an RMS bigger than 1.2 and less than 1.8. The relationships between the three-dimensional structure and functionality are potentially difficult to predict in this region of the TY145 like subtilases.

The nonhomologous region consists of residues 5-15, 16-23, 86-87, 129-133, 197-201, 213-224, 285-286, 291-298 and 299-311. The nonhomologous region has a RMS higher than 1.5, which also pertains to residues 65-66 from the intermediate region. The group comprising residues 5-15 and 299-311 has an RMS between 2.1-2.2. The relationships between the three-dimensional structure and functionality are very difficult to predict in this region of the TY145 like subtilases.

The regions in areas A1-T5, N16-T24, A46-Q51, S58-C66, G84-G90, S129-K134, S129-K134, S173-S175, V196-T201, N212-R224, A284-V286, K290-D299 and V310-K311 in the TY145 structure differs significantly from the other S8 family subtilisins (including the BPN' type subtilisins) in c-alpha atom coordinates. An RMS cannot be calculated for these last
 5 residues as there are no homologous c-alpha atoms in the compared subtilases.

Homology building of TY145 and BPN' like subtilases

A model structure of a TY145 like subtilase or a BPN' like subtilase can be built using the Homology program or a comparable program, e.g., Modeller (both from Molecular Simula-
 10 tions, Inc., San Diego, CA). The principle is to align the amino acid sequence of a protein for which the 3D structure is known with the amino acid sequence of a protein for which a model 3D structure has to be constructed. The structurally conserved regions can then be built on the basis of consensus sequences. In areas lacking homology, loop structures can be inserted, or sequences can be deleted with subsequent bonding of the necessary resi-
 15 dues using, e.g., the program Homology. Subsequent relaxing and optimization of the structure should be done using either Homology or another molecular simulation program, e.g., CHARMM from Molecular Simulations.

Methods for designing TY145 and Subtilisin family subtilase variants

20 Comparisons of the molecular dynamics of different proteins can give a hint as to which domains are important or connected to certain properties pertained by each protein.

The present invention comprises a method of producing a variant of a parent TY145 like subtilase, the variant having at least one altered property as compared to the parent TY145
 25 like subtilase, the method comprising:

- a) modelling the parent TY145 subtilase on the three-dimensional structure of a TY145 subtilase to produce a three-dimensional structure of the parent TY145 subtilase;
- b) identifying on the basis of the comparison in step a) at least one structural part of the parent TY145 subtilase, wherein an alteration in said structural part is predicted to re-
 30 sult in an altered property;
- c) modifying the nucleic acid sequence encoding the parent TY145 subtilase to produce a nucleic acid sequence encoding deletion or substitution of one or more amino acids at a position corresponding to said structural part, or an insertion of one or more amino acid residues in positions corresponding to said structural part;

- d) expressing the modified nucleic acid sequence in a host cell to produce the variant TY145 subtilase;
- e) isolating the produced subtilase;
- f) purifying the isolated subtilase and
- 5 g) recovering the purified subtilase.

Further the present invention comprises a method of producing a variant of a parent Subtilisin family subtilase, such as a BPN' like subtilase, the variant having at least one altered property as compared to the parent Subtilisin family subtilase, the method comprising:

- 10 a) modelling the parent Subtilisin family subtilase on the three-dimensional structure of a Subtilisin family subtilase to produce a three-dimensional structure of the parent Subtilisin family subtilase;
- b) comparing the three-dimensional structure obtained in step a) to the three-dimensional structure of a TY145 like subtilase;
- 15 c) identifying on the basis of the comparison in step b) at least one structural part of the parent Subtilisin family subtilase, wherein an alteration in said structural part is predicted to result in an altered property;
- d) modifying the nucleic acid sequence encoding the parent Subtilisin family subtilase to produce a nucleic acid sequence encoding deletion or substitution of one or more
- 20 amino acids at a position corresponding to said structural part, or an insertion of one or more amino acid residues in positions corresponding to said structural part;
- e) expressing the modified nucleic acid sequence in a host cell to produce the variant Subtilisin family subtilase,
- f) isolating the produced subtilase,
- 25 g) purifying the isolated subtilase and
- h) recovering the purified subtilase.

Further the present invention comprises a method of producing a variant of a parent TY145 like subtilase, the variant having at least one altered property as compared to the parent

- 30 TY145 like subtilase, the method comprising:
 - a) modelling the parent TY145 like subtilase on the three-dimensional structure of a TY145 like subtilase to produce a three-dimensional structure of the parent TY145 like subtilase;
 - b) comparing the three-dimensional structure obtained in step a) to the three-dimensional
 - 35 structure of a Subtilisin family subtilase;

- c) identifying on the basis of the comparison in step b) at least one structural part of the parent TY145 like subtilase, wherein an alteration in said structural part is predicted to result in an altered property;
- d) modifying the nucleic acid sequence encoding the parent TY145 like subtilase to produce a nucleic acid sequence encoding deletion or substitution of one or more amino acids at a position corresponding to said structural part, or an insertion of one or more amino acid residues in positions corresponding to said structural part;
- e) expressing the modified nucleic acid sequence in a host cell to produce the variant TY145 like subtilase;
- f) isolating the produced subtilase;
- g) purifying the isolated subtilase and
- h) recovering the purified subtilase.

Stability - alteration of ion-binding sites

As described above the TY145 subtilases has two new ion-binding sites not present in the BPN' subtilisin structures but lacks the Strong ion-binding site of the BPN' subtilases. Stability of the ion-binding site is of crucial importance for the functionality of the enzyme. Therefore alterations of the amino acid residues close to the ion-binding sites are likely to result in alterations of the stability of the enzyme.

The positions which may be modified are located at:

Weak: 10Å around calcium atom named C 314,

Near: 10Å around calcium atom named C 312, and

Far: 10Å around calcium atom named C 313 in the PDB table (Appendix 1).

Improved stability

Stabilisation of the ion-binding sites of TY145 may possibly be obtained by alterations in the positions close to the sites. Positions located at a distance of 10Å to the ion-binding sites of TY145 (SEQ ID NO:1) are:

Weak: 154, 155, 158, 164, 165, 166, 167, 168, 178-191 (i.e. 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191), 211, 220-228 (i.e. 220, 221, 222, 223, 224, 225, 226, 227, 228), 277, 281 and 305.

Near: 185, 211-227 (i.e. 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227), 277, 281, 299, 300, 301, 304, 305.

Far: 193, 198, 199, 201, 202, 204, 216, 217, 219, 226, 227, 228, 229 and 284-307 (i.e. 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307).

- 5 In detergent compositions calcium chelaters contribute to removal of calcium from the subtilases with subsequent inactivation of the enzyme as the result. To decrease the inactivation due to calcium removal of e.g. calcium chelaters, variants with improved calcium stability can be constructed.

10 Variants with alterations close to the Near ion-binding site are I220S,T and T215S, variants with alterations close to the Far ion-binding site are G298A,S,T and G296A,S,T, and variants with alterations close to the Weak ion-binding site are V185T and I221N,D,T.

TY145 with extra ion-binding site

15 The Strong ion-binding site from the BPN' subtilases can be transplanted into TY145 (or other subtilases in TY145 subgroup) by deletion of or in the region H83-G90 (of SEQ ID NO:1) and subsequent insertion of one or more amino acid residues. A preferred variant has the whole region deleted and a subsequent insertion between A82 and V91 of the sequence LNNSIG.

20 Removal of ion-binding site in TY145

By removing a ion-binding site it is possible to alter the enzymes dependency of calcium or other ions in the solution. The Far and Near ion-binding sites in TY145 (or others from TY145 group) can be removed with guidance from the three-dimensional structure of BPN' and Savinase (or others in BPN' group).

25 Removal of the Far site can be done by deletion of or in the region K290-D300 (of SEQ ID NO:1) and subsequent insertion of one or more amino acid residues. A preferred variant has the whole region deleted and a subsequent insertion between I289 and Y301 of the sequence GDS or DST. Preferably, but not mandatory the substitution S303Y is further added.

30 Removal of the Near site can be done by deletion of or in the region N212-R224 (of SEQ ID NO:1) and subsequent insertion of one or more amino acid residues. A preferred variant has the whole region deleted and a subsequent insertion of a proline or alanine residue between G211 and D225.

Removal of Strong ion-binding site in BPN' subtilases

The Strong ion-binding site in BPN' like subtilases can be removed. Exemplified in Savinase, the removal can be done by deletion of or in the region L75-G80 (BPN' numbering) and subsequent insertion of one or more amino acid residues. A preferred variant has the whole region deleted and a subsequent insertion of residues 84-88 from TY145. In addition the substitutions L82Y and Q2A,N can be applied.

Alteration of thermostability

A variant with improved stability (typically increased thermostability) may be obtained by substitution with proline, introduction of a disulfide bond, altering a hydrogen bond contact, altering charge distribution, introduction of a salt bridge, filling in an internal structural cavity with one or more amino acids with bulkier side groups (in e.g. regions which are structurally mobile), substitution of histidine residues with other amino acids, removal of a deamidation sites, or by helix capping.

Regions with increased mobility:

The following regions of TY145 have an increased mobility in the crystal structure of the enzyme, and it is presently believed that these regions can be responsible for stability or activity of TY145. Especially thermostabilisation may possibly be obtained by altering the highly mobile regions. Improvements of the enzyme can be obtained by mutation in the below regions and positions. Introducing e.g. larger residues or residues having more atoms in the side chain could increase the stability, or, e.g., introduction of residues having fewer atoms in the side chain could be important for the mobility and thus the activity profile of the enzyme. The regions can be found by analysing the B-factors taken from the coordinate file in Appendix 1, and/or from molecular dynamics calculations of the isotropic fluctuations. These can be obtained by using the program CHARMM from MSI (Molecular Simulations Inc.).

Molecular dynamics simulation at 300K of TY145 reveals the following highly mobile regions:

84-89 (i.e. 84, 85, 86, 87, 88)

108-117 (i.e. 108, 109, 110, 111, 112, 113, 114, 115, 116, 117)

141-146 (i.e. 141, 142, 143, 144, 145, 146)

150-152 (i.e. 150, 151, 152)

169-171 (i.e. 169, 170, 171)

200-201

211-220 (i.e. 211, 212, 213, 214, 215, 216, 217, 218, 219, 220)

242-243

268-270 (i.e. 268, 269, 270).

5

Also B-factors (see "in X-Ray Structure Determination, Stout, G.K. and Jensen, L.H., John Wiley & Sons, Inc. NY, 1989") from crystallographic data indicates the following more mobile regions in the TY145 structure:

1-7 (i.e. 1, 2, 3, 4, 5, 6, 7),

10 17-23 (i.e. 17, 18, 19, 20, 21, 22, 23),

38-50 (i.e. 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50),

57-69 (i.e. 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69),

84-92 (i.e. 84, 85, 86, 87, 88, 89, 90, 91, 92),

107-110 (i.e. 107, 108, 109, 110),

15 239-243 (i.e. 239, 240, 241, 242, 243) and

265-266.

Preferably the regions 57-69 and 84-92.

Disulfide bonds:

20 A TY145 variant of the present invention with improved stability, e.g. thermostability, as compared to the parent TY145 may be obtained by introducing new inter-domain or intra-domain bonds, such as by establishing inter- or intra-domain disulfide bridges.

Thus a further aspect of the present invention relates to a method for producing a variant of a parent TY145 comprising the methods described in the paragraph "Methods of preparing

25 TY145 like or BPN' like subtilase variants" herein.

According to the guidelines mentioned above the below mentioned amino acid residues identified in the amino acid sequence of SEQ ID NO:1 are contemplated as being suitable for cysteine replacement. With one or more of these substitutions with cysteine, disulfide

30 bridges may possibly form in a variant of TY145. The substitutions are: G26C + A95C; A167C + T254C; R203C + G292C and V228C + A284C.

Similar residues suitable for cysteine replacement in homologous subtilases such as TA39, TA41 can be elucidated by finding the homologous positions in the alignment of Figure 1.

35 Concerning another TY145 like sequence the homologous positions suitable for cysteine

replacement can be selected by aligning said TY145 like sequence with all of the sequences of Figure 1 using the GAP analysis method as described above. The suitable residues can then be selected in accordance with the homologous positions in the most homologous of SEQ ID's NO:1,2,3 and 4 which are the sequences of the subtilases aligned in Figure 1.

Surface charge distribution

A variant with improved stability (typically improved thermostability) as compared to the parent subtilase may be obtained by changing the surface charge distribution of the subtilase. For example, when the pH is lowered to about 5 or below histidine residues typically become positively charged and, consequently, unfavorable electrostatic interactions on the protein surface may occur. By engineering the surface charge of the subtilase one may avoid such unfavorable electrostatic interactions that in turn lead to a higher stability of the subtilase.

Therefore, a further aspect of the present invention relates to method for constructing a variant of a parent subtilase, the method comprising:

- a) identifying, on the surface of the parent subtilase, preferably a TY145 like or a BPN' like subtilase, at least one amino acid residue selected from the group consisting of Asp, Glu, Arg, Lys and His;
- b) substituting, on the surface of the parent subtilase, at least one amino acid residue selected from the group consisting of Asp, Glu, Arg, Lys and His with an uncharged amino acid residue;
- c) optionally repeating steps a) and b) recursively;
- d) optionally, making alterations each of which is an insertion, a deletion or a substitution of an amino acid residue at one or more positions other than b);
- e) preparing the variant resulting from steps a) - d);
- f) testing the stability of said variant; and
- g) optionally repeating steps a) - f) recursively; and
- h) selecting a subtilase variant having increased stability as compared to the parent subtilase.

As will be understood by the skilled person it may also, in some cases, be advantageous to substitute an uncharged amino acid residue with an amino acid residue bearing a charge or, alternatively, it may in some cases be advantageous to substitute an amino acid residue

bearing a charge with an amino acid residue bearing a charge of opposite sign. Thus, the above-mentioned method may easily be employed by the skilled person also for these purposes. In the case of substituting an uncharged amino acid residue with an amino acid residue bearing a charge the above-mentioned method may be employed the only difference being steps a) and b) which will then read:

- a) identifying, on the surface of the parent subtilase, at least one uncharged amino acid residue;
- b) substituting, on the surface of the parent subtilase, at least one uncharged amino acid residue with a charged amino acid residue selected from the group consisting of Asp, Glu, Arg, Lys and His.

Also in the case of changing the sign of an amino acid residue present on the surface of the subtilase the above method may be employed. Again, compared to the above method, the only difference being steps a) and b) which, in this case, read:

- a) identifying, on the surface of the parent subtilase, at least one charged amino acid residue selected from the group consisting of Asp, Glu, Arg, Lys and His;
- b) substituting, on the surface of the parent subtilase, at least one charged amino acid residue identified in step a) with an amino acid residue having an opposite charge.

Thus, Asp may be substituted with Arg, Lys or His; Glu may be substituted with Arg, Lys or His; Arg may be substituted with Asp or Glu; Lys may be substituted with Asp or Glu; and His may be substituted with Asp or Glu.

In order to determine the amino acid residues of a subtilase, which are present on the surface of the enzyme, the surface accessible area are measured using the DSSP program (Kabsch and Sander, *Biopolymers* (1983), 22, 2577-2637). All residues having a surface accessibility higher than 0 is regarded a surface residue.

An amino acid residue found on the surface of TY145 using the above method is D116 and it is contemplated that the substitutions D116H,K,R are of particular interest.

Similar substitutions may be introduced in equivalent positions of other TY145 like subtilases.

Substitution with proline residues

Improved thermostability of a subtilase can be obtained by subjecting the subtilase in question to analysis for secondary structure, identifying residues in the subtilase having dihedral angles ϕ (phi) and ψ (psi) confined to the intervals $[-90^\circ < \phi < -40^\circ$ and $-180^\circ < \psi < 180^\circ]$, preferably

ly the intervals $[-90^\circ < \phi < -40^\circ$ and $120^\circ < \psi < 180^\circ]$ or $[-90^\circ < \phi < -40^\circ$ and $-50^\circ < \psi < 10^\circ]$ and excluding residues located in regions in which the subtilase is characterized by possessing α -helical or β -sheet structure.

After the dihedral angles ϕ (phi) and ψ (psi) for the amino acids have been calculated, based on the atomic structure in the crystalline subtilases, it is possible to select position(s) which has/have dihedral phi and psi angles favourable for substitution with a proline residue. The aliphatic side chain of proline residues is bonded covalently to the nitrogen atom of the peptide group. The resulting cyclic five-membered ring consequently imposes a rigid constraint on the rotation about the N-C α bond of the peptide backbone and simultaneously prevents the formation of hydrogen bonding to the backbone N-atom. For these structural reasons, proline residues are generally not compatible with α -helical and β -sheet secondary conformations.

If a proline residue is not already at the identified position(s), the naturally occurring amino acid residue is substituted with a proline residue, preferably by site directed mutagenesis applied on a gene encoding the subtilase in question.

In the group of TY145 like subtilases proline residues can be introduced at positions 18, 115, 185, 269 and 293. Accordingly, a preferred TY145 variant has one or more of the substitutions: Q18P, D115P, V185P, T269P and I293P.

Alteration of activity

Introduction of activity at low temperature in TY145 and Savinase

A comparison of the molecular dynamics at 300K of TY145 (a mesophilic-derived enzyme obtained from crystal structure) and TA41 (a psychrophilic derived enzyme obtained from modelling) was conducted.

The comparison was directed to low temperature activity and revealed a difference in dynamical behaviour of TY145 and TA41. The theory derived from the comparison is that the difference in dynamics, especially around the active site, are important for the low temperature functionality of the psychrophilic enzyme. The necessary dynamics are needed for the enzyme to have activity at low temperature and thus the activity drops if the enzymes dynamics are lowered.

The higher mobility regions in TA41 compared to TY145 measured by molecular dynamics simulation indicates important regions for the low temperature activity, of the enzyme TA41 which can be transferred to TY145.

The regions in TA41 are:

16-22 (i.e. 16, 17, 18, 19, 20, 21, 22),

40-73 (i.e. 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73),
 118-131 (i.e. 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131)
 140-161 (i.e. 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154,
 5 155, 156, 157, 158, 159, 160, 161) and
 275-294 (i.e. 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289,
 290, 291, 292, 293, 294).

Regions closest to the active site and the substrate binding site are regarded as preferred
 10 in relation to making higher activity at low temperature for TY145: 40-73, and 140-161,
 preferably 65-73 and 140-150. The regions in TY145 should be modified to be more mobile
 for example by substitution with small less rigid residues, i.e. residues with smaller side
 chains (such as Gly, Ala, Ser, Thr or Val), into the TY145 backbone.
 The other regions in TA41 are most interesting for stabilisation of the psychrophilic en-
 15 zyme. These regions can easily be found in TA39 as well or in other homologous enzymes,
 also non psychrophilics.

The regions around the active site and the substrate binding site are the regions most likely
 involved in the low temperature functionality.

20 Below are suggestions for transferring the low temperature activity of TA41 and homolo-
 gous sequences to TY145-like sequences and the BPN'-like sequences:

	<u>TA41</u>	<u>TY145</u>	<u>Savinase</u>
	I31	V31	V28I,A,L
25	V38	V38	I35V,A,L
	S79	T79	T71S
	A80	V80	I72A,G,V
	L81	L81	A73L,G
	V187	V188	M175V,A
30	T253	T254	T224S,A

The numbering is according to SEQ ID NO:3, 1 and 5 respectively. Savinase is numbered
 according to BPN'.

Preferred Savinase variants are V28I, I35V, T71S, I72A, A73L, M175V and T224S.

35 Examples of core variants of TY145 are: V31I, V80A, T79S.

The alterations of the TY145-like sequences and the BPN'-like sequences can be single mutations or combinations of the suggested mutations.

Substrate bindings site

5 The substrate binding site is identified by the residues in contact with a substrate model, such as the CI2 inhibitor. The 3D structure coordinates of the TY145 subtilase with CI2 bound in the active site can be found in Appendix 1. Without being limited to any theory, it is presently believed that binding between a substrate and an enzyme is supported by favorable interactions found within a sphere 10 Å from the substrate molecule, in particular
10 within a sphere of 6 Å from the substrate molecule. Examples of such favorable bonds are hydrogen bonds, strong electrostatic interaction and/or hydrophobic interactions. The following residues of the TY145 subtilase (SEQ ID NO:1), are within a distance of 6Å from the CI2 inhibitor and thus believed to be involved in interactions with said substrate:
15 35,36,70,72,106,109,110,111,112,113,114,117,139,140,141,142,143,144,145,147,150,167,168,169,170,171,172,173,174,177,180,207,239,247,148,149,150,151 and 252.

Combined modifications

The present invention also encompasses any of the above mentioned subtilase variants in combination with any other modification to the amino acid sequence thereof. Especially
20 combinations with other modifications known in the art to provide improved properties to the enzyme are envisaged.

Such combinations comprise the positions: 222 (improves oxidation stability), 218 (improves thermal stability), substitutions in the Ca²⁺-binding sites stabilizing the enzyme, e.g. position 76, and many other apparent from the prior art.

25 In further embodiments a subtilase variant described herein may advantageously be combined with one or more modification(s) in any of the positions:

27, 36, 56, 76, 87, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 120, 123, 159, 167, 170,
30 206, 218, 222, 224, 232, 235, 236, 245, 248, 252 and 274 (BPN' numbering).

Specifically, the following BLSAVI, BLSUBL, BSKSMK, and BAALKP modifications are considered appropriate for combination:

35 K27R, *36D, S56P, N76D, S87N, G97N, S101G, S103A, V104A, V104I, V104N, V104Y,

H120D, N123S, G159D, Y167, R170, Q206E, N218S, M222S, M222A, T224S, A232V, K235L, Q236H, Q245R, N248D, N252K and T274A.

Furthermore variants comprising any of the modifications S101G+V104N, S87N+S101G+V104N, K27R+V104Y+N123S+T274A, N76D+S103A+V104I or N76D+V104A, or other combinations of the modifications K27R, N76D, S101G, S103A, V104N, V104Y, V104I, V104A, N123S, G159D, A232V, Q236H, Q245R, N248D, N252K, T274A in combination with any one or more of the modification(s) mentioned above exhibit improved properties.

- 10 A particular interesting variant is a variant, which, in addition to modifications according to the invention, contains the following substitutions:
S101G+S103A+V104I+G159D+A232V+Q236H+Q245R+N248D+N252K.

- Moreover, subtilase variants of the main aspect(s) of the invention are preferably combined with one or more modification(s) in any of the positions 129, 131 and 194, preferably as 129K, 131H and 194P modifications, and most preferably as P129K, P131H and A194P modifications. Any of those modification(s) are expected to provide a higher expression level of the subtilase variant in the production thereof.

20 **Stabilization by modification of Asn-Gly pairs**

- It is known that at alkaline pH, the side chain of Asn may interact with the NH group of a sequential neighbouring amino acid to form an isoAsp residue where the backbone goes through the Asp side chain. This will leave the backbone more vulnerable to proteolysis. The deamidation is much more likely to occur if the residue that follows is a Gly. Changing the Asn in front of the Gly or the Gly will prevent this from happening and thus improve the stability, especially as concerns thermo- and storage stability.

- The invention consequently further relates to a subtilase, in which either or both residues of any of the Asn-Gly sequence appearing in the amino acid sequence of the parent RP-II protease is/are deleted or substituted with a residue of a different amino acid.

The Asn and/or Gly residue may, for instance, be substituted with a residue of an amino acid selected from the group consisting of A, Q, S, P, T and Y.

Modification of Tyrosine residues

In relation to wash performance it has been found that the modification of certain tyrosine residues to phenylalanine provides an improved wash performance. Without being bound by any specific theory, it is believed that titration of these Tyr residues in the alkaline wash liquor
5 has negative effects that are alleviated by replacing the Tyr residues with other residues, especially Phe or Trp, particularly Phe.

Methods of preparing TY145 like or BPN' like subtilase variants

The subtilase variants, i.e. the TY145 and BPN' variants of the present invention may be
10 produced by any known method within the art and the present invention also relates to nucleic acid encoding a subtilase variant of the present invention, a DNA construct comprising said nucleic acid and a host cell comprising said nucleic acid sequence.

In general natural occurring proteins may be produced by culturing the organism expressing the protein and subsequently purifying the protein or it may be produced by cloning a
15 nucleic acid, e.g. genomic DNA or cDNA, encoding the protein into an expression vector, introducing said expression vector into a host cell, culturing the host cell and purifying the expressed protein.

Typically protein variants may be produced by site-directed mutagenesis of a parent protein, introduction into expression vector, host cell etc. The parent protein may be cloned
20 from a strain producing the polypeptide or from an expression library, i.e. it may be isolated from genomic DNA or prepared from cDNA, or a combination thereof.

In general standard procedures for cloning of genes and/or introducing mutations (random and/or site directed) into said genes may be used in order to obtain a parent subtilase, or subtilase or subtilase variant of the invention. For further description of suitable techniques
25 reference is made to Molecular cloning: A laboratory manual (Sambrook et al. (1989), Cold Spring Harbor lab., Cold Spring Harbor, NY; Ausubel, F. M. et al. (eds.)); Current protocols in Molecular Biology (John Wiley and Sons, 1995; Harwood, C. R., and Cutting, S. M. (eds.)); Molecular Biological Methods for Bacillus (John Wiley and Sons, 1990); DNA Cloning: A Practical Approach, Volumes I and II (D.N. Glover ed. 1985); Oligonucleotide Synthesis (M.J. Gait ed. 1984); Nucleic Acid Hybridization (B.D. Hames & S.J. Higgins eds (1985)); Transcription And Translation (B.D. Hames & S.J. Higgins, eds. (1984)); Animal Cell Culture (R.I. Freshney, ed. (1986)); Immobilized Cells And Enzymes (IRL Press, (1986)); A Practical Guide To Molecular Cloning (B. Perbal, (1984)) and WO 96/34946.

35 Further, variants could be constructed by:

Random Mutagenesis

Random mutagenesis is suitably performed either as localized or region-specific random mutagenesis in at least three parts of the gene translating to the amino acid sequence shown in question, or within the whole gene.

The random mutagenesis of a DNA sequence encoding a parent subtilase may be conveniently performed by use of any method known in the art.

In relation to the above, a further aspect of the present invention relates to a method for generating a variant of a parent subtilase, wherein the variant exhibits an altered property, such as increased thermostability, increased stability at low pH and at low calcium concentration, relative to the parent subtilase, the method comprising:

- (a) subjecting a DNA sequence encoding the parent subtilase to random mutagenesis,
- (b) expressing the mutated DNA sequence obtained in step (a) in a host cell, and
- (c) screening for host cells expressing a subtilase variant which has an altered property relative to the parent subtilase.

Step (a) of the above method of the invention is preferably performed using doped primers. For instance, the random mutagenesis may be performed by use of a suitable physical or chemical mutagenizing agent, by use of a suitable oligonucleotide, or by subjecting the DNA sequence to PCR generated mutagenesis. Furthermore, the random mutagenesis may be performed by use of any combination of these mutagenizing agents. The mutagenizing agent may, e.g., be one which induces transitions, transversions, inversions, scrambling, deletions, and/or insertions.

Examples of a physical or chemical mutagenizing agent suitable for the present purpose include ultraviolet (UV) irradiation, hydroxylamine, N-methyl-N'-nitro-N-nitrosoguanidine (MNNG), O-methyl hydroxylamine, nitrous acid, ethyl methane sulphonate (EMS), sodium bisulphite, formic acid, and nucleotide analogues. When such agents are used, the mutagenesis is typically performed by incubating the DNA sequence encoding the parent enzyme to be mutagenized in the presence of the mutagenizing agent of choice under suitable conditions for the mutagenesis to take place, and selecting for mutated DNA having the desired properties.

When the mutagenesis is performed by the use of an oligonucleotide, the oligonucleotide may be doped or spiked with the three non-parent nucleotides during the synthesis of the oligonucleotide at the positions that are to be changed. The doping or spiking may be done so that codons for unwanted amino acids are avoided. The doped or spiked oligonucleotide

can be incorporated into the DNA encoding the subtilase enzyme by any published technique, using, e.g., PCR, LCR or any DNA polymerase and ligase as deemed appropriate. Preferably, the doping is carried out using "constant random doping", in which the percentage of wild-type and modification in each position is predefined. Furthermore, the doping may be directed toward a preference for the introduction of certain nucleotides, and thereby a preference for the introduction of one or more specific amino acid residues. The doping may be made, e.g., so as to allow for the introduction of 90% wild type and 10% modifications in each position. An additional consideration in the choice of a doping scheme is based on genetic as well as protein-structural constraints. The doping scheme may be made by using the DOPE program which, *inter alia*, ensures that introduction of stop codons is avoided (L.J. Jensen et al. *Nucleic Acid Research*, 26, 697-702 (1998)).

When PCR-generated mutagenesis is used, either a chemically treated or non-treated gene encoding a parent subtilase enzyme is subjected to PCR under conditions that increase the misincorporation of nucleotides (Deshler 1992; Leung et al., *Technique*, 1, 1989, pp. 11-15).

A mutator strain of *E. coli* (Fowler et al., *Molec. Gen. Genet.*, 133, 1974, 179-191), *S. cerevisiae* or any other microbial organism may be used for the random mutagenesis of the DNA encoding the subtilase by, e.g., transforming a plasmid containing the parent enzyme into the mutator strain, growing the mutator strain with the plasmid and isolating the mutated plasmid from the mutator strain. The mutated plasmid may be subsequently transformed into the expression organism.

The DNA sequence to be mutagenized may conveniently be present in a genomic or cDNA library prepared from an organism expressing the parent subtilase. Alternatively, the DNA sequence may be present on a suitable vector such as a plasmid or a bacteriophage, which as such may be incubated with or otherwise exposed to the mutagenising agent. The DNA to be mutagenized may also be present in a host cell either by being integrated in the genome of said cell or by being present on a vector harbored in the cell. Finally, the DNA to be mutagenized may be in isolated form. It will be understood that the DNA sequence to be subjected to random mutagenesis is preferably a cDNA or a genomic DNA sequence.

In some cases it may be convenient to amplify the mutated DNA sequence prior to performing the expression step b) or the screening step c). Such amplification may be performed in accordance with methods known in the art, the presently preferred method being PCR-generated amplification using oligonucleotide primers prepared on the basis of the DNA or amino acid sequence of the parent enzyme.

Subsequent to the incubation with or exposure to the mutagenising agent, the mutated DNA is expressed by culturing a suitable host cell carrying the DNA sequence under conditions allowing expression to take place. The host cell used for this purpose may be one which has been transformed with the mutated DNA sequence, optionally present on a vector, or one which was carried the DNA sequence encoding the parent enzyme during the mutagenesis treatment. Examples of suitable host cells are the following: gram positive bacteria such as *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus lentus*, *Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus coagulans*, *Bacillus circulans*, *Bacillus lautus*, *Bacillus megaterium*, *Bacillus thuringiensis*, *Streptomyces lividans* or *Streptomyces murinus*; and gram negative bacteria such as *E. coli*. The mutated DNA sequence may further comprise a DNA sequence encoding functions permitting expression of the mutated DNA sequence.

Localised random mutagenesis

The random mutagenesis may be advantageously localised to a part of the parent subtilase in question. This may, e.g., be advantageous when certain regions of the enzyme have been identified to be of particular importance for a given property of the enzyme, and when modified are expected to result in a variant having improved properties. Such regions may normally be identified when the tertiary structure of the parent enzyme has been elucidated and related to the function of the enzyme.

The localised or region-specific, random mutagenesis is conveniently performed by use of PCR generated mutagenesis techniques as described above or any other suitable technique known in the art. Alternatively, the DNA sequence encoding the part of the DNA sequence to be modified may be isolated, e.g., by insertion into a suitable vector, and said part may be subsequently subjected to mutagenesis by use of any of the mutagenesis methods discussed above.

General method for random mutagenesis by use of the DOPE program

The random mutagenesis may be carried out by the following steps:

1. Select regions of interest for modification in the parent enzyme
2. Decide on mutation sites and non-mutated sites in the selected region
3. Decide on which kind of mutations should be carried out, e.g. with respect to the desired stability and/or performance of the variant to be constructed
4. Select structurally reasonable mutations
5. Adjust the residues selected by step 3 with regard to step 4.

6. Analyse by use of a suitable dope algorithm the nucleotide distribution.
7. If necessary, adjust the wanted residues to genetic code realism, e.g. taking into account constraints resulting from the genetic code, e.g. in order to avoid introduction of stop codons; the skilled person will be aware that some codon combinations cannot be used in practice and will need to be adapted
8. Make primers
9. Perform random mutagenesis by use of the primers
10. Select resulting subtilase variants by screening for the desired improved properties.

10 Suitable dope algorithms for use in step 6 are well known in the art. One such algorithm is described by Tomandl, D. et al., 1997, Journal of Computer-Aided Molecular Design 11:29-38. Another algorithm is DOPE (Jensen, LJ, Andersen, KV, Svendsen, A, and Kretzschmar, T (1998) Nucleic Acids Research 26:697-702).

15 Expression vectors

A recombinant expression vector comprising a nucleic acid sequence encoding a subtilase variant of the invention may be any vector that may conveniently be subjected to recombinant DNA procedures and which may bring about the expression of the nucleic acid sequence.

20 The choice of vector will often depend on the host cell into which it is to be introduced. Examples of a suitable vector include a linear or closed circular plasmid or a virus. The vector may be an autonomously replicating vector, i.e., a vector which exists as an extra-chromosomal entity, the replication of which is independent of chromosomal replication, e.g., a plasmid, an extra-chromosomal element, a mini chromosome, or an artificial chromosome. The vector may contain any means for assuring self-replication. Examples of bacterial origins of replication are the origins of replication of plasmids pBR322, pUC19, pACYC177, pACYC184, pUB110, pE194, pTA1060, and pAM β 1. Examples of origin of replications for use in a yeast host cell are the 2 micron origin of replication, the combination of CEN6 and ARS4, and the combination of CEN3 and ARS1. The origin of replication may be one having a mutation which makes it function as temperature-sensitive in the host cell (see, e.g., Ehrlich, 1978, Proceedings of the National Academy of Sciences USA 75:1433).

Alternatively, the vector may be one which, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. Vectors which are integrated into the genome of the host cell may contain any

nucleic acid sequence enabling integration into the genome, in particular it may contain nucleic acid sequences facilitating integration into the genome by homologous or non-homologous recombination. The vector system may be a single vector, e.g. plasmid or virus, or two or more vectors, e.g. plasmids or virus', which together contain the total DNA to be introduced into the genome of the host cell, or a transposon.

The vector may in particular be an expression vector in which the DNA sequence encoding the subtilase variant of the invention is operably linked to additional segments or control sequences required for transcription of the DNA. The term, "operably linked" indicates that the segments are arranged so that they function in concert for their intended purposes, e.g. transcription initiates in a promoter and proceeds through the DNA sequence encoding the subtilase variant. Additional segments or control sequences include a promoter, a leader, a polyadenylation sequence, a propeptide sequence, a signal sequence and a transcription terminator. At a minimum the control sequences include a promoter and transcriptional and translational stop signals.

The promoter may be any DNA sequence that shows transcriptional activity in the host cell of choice and may be derived from genes encoding proteins either homologous or heterologous to the host cell.

Examples of suitable promoters for use in bacterial host cells include the promoter of the *Bacillus subtilis* levansucrase gene (sacB), the *Bacillus stearothermophilus* maltogenic amylase gene (amyM), the *Bacillus licheniformis* alpha-amylase gene (amyL), the *Bacillus amyloliquefaciens* alpha-amylase gene (amyQ), the *Bacillus subtilis* alkaline protease gene, or the *Bacillus pumilus* xylosidase gene, the *Bacillus amyloliquefaciens* BAN amylase gene, the *Bacillus licheniformis* penicillinase gene (penP), the *Bacillus subtilis* xylA and xylB genes, and the prokaryotic beta-lactamase gene (Villa-Kamaroff et al., 1978, Proceedings of the National Academy of Sciences USA 75:3727-3731). Other examples include the phage Lambda P_R or P_L promoters or the E. coli lac, trp or tac promoters or the *Streptomyces coelicolor* agarase gene (dagA). Further promoters are described in "Useful proteins from recombinant bacteria" in Scientific American, 1980, 242:74-94; and in Sambrook et al., 1989, supra.

Examples of suitable promoters for use in a filamentous fungal host cell are promoters obtained from the genes encoding *Aspergillus oryzae* TAKA amylase, *Rhizomucor miehei* aspartic proteinase, *Aspergillus niger* neutral alpha-amylase, *Aspergillus niger* acid stable alpha-amylase, *Aspergillus niger* or *Aspergillus awamori* glucoamylase (glaA), *Rhizomucor miehei* lipase, *Aspergillus oryzae* alkaline protease, *Aspergillus oryzae* triose phosphate isomerase, *Aspergillus nidulans* acetamidase, *Fusarium oxysporum* trypsin-like protease

(as described in U.S. Patent No. 4,288,627, which is incorporated herein by reference), and hybrids thereof. Particularly preferred promoters for use in filamentous fungal host cells are the TAKA amylase, NA2-tpi (a hybrid of the promoters from the genes encoding *Aspergillus niger* neutral (-amylase and *Aspergillus oryzae* triose phosphate isomerase), and glaA promoters. Further suitable promoters for use in filamentous fungus host cells are the ADH3 promoter (McKnight et al., The EMBO J. 4 (1985), 2093 - 2099) or the tpiA promoter. Examples of suitable promoters for use in yeast host cells include promoters from yeast glycolytic genes (Hitzeman et al., J. Biol. Chem. 255 (1980), 12073 - 12080; Alber and Kawasaki, J. Mol. Appl. Gen. 1 (1982), 419 - 434) or alcohol dehydrogenase genes (Young et al., in Genetic Engineering of Microorganisms for Chemicals (Hollaender et al, eds.), Plenum Press, New York, 1982), or the TPI1 (US 4,599,311) or ADH2-4c (Russell et al., Nature 304 (1983), 652 - 654) promoters.

Further useful promoters are obtained from the *Saccharomyces cerevisiae* enolase (ENO-1) gene, the *Saccharomyces cerevisiae* galactokinase gene (GAL1), the *Saccharomyces cerevisiae* alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase genes (ADH2/GAP), and the *Saccharomyces cerevisiae* 3-phosphoglycerate kinase gene. Other useful promoters for yeast host cells are described by Romanos et al., 1992, Yeast 8:423-488. In a mammalian host cell, useful promoters include viral promoters such as those from Simian Virus 40 (SV40), Rous sarcoma virus (RSV), adenovirus, and bovine papilloma virus (BPV).

Examples of suitable promoters for use in mammalian cells are the SV40 promoter (Subramani et al., Mol. Cell Biol. 1 (1981), 854 -864), the MT-1 (metallothionein gene) promoter (Palmiter et al., Science 222 (1983), 809 - 814) or the adenovirus 2 major late promoter.

An example of a suitable promoter for use in insect cells is the polyhedrin promoter (US 4,745,051; Vasuvedan et al., FEBS Lett. 311, (1992) 7 - 11), the P10 promoter (J.M. Vlak et al., J. Gen. Virology 69, 1988, pp. 765-776), the Autographa californica polyhedrosis virus basic protein promoter (EP 397 485), the baculovirus immediate early gene 1 promoter (US 5,155,037; US 5,162,222), or the baculovirus 39K delayed-early gene promoter (US 5,155,037; US 5,162,222).

The DNA sequence encoding a subtilase variant of the invention may also, if necessary, be operably connected to a suitable terminator.

The recombinant vector of the invention may further comprise a DNA sequence enabling the vector to replicate in the host cell in question.

The vector may also comprise a selectable marker, e.g. a gene the product of which complements a defect in the host cell, or a gene encoding resistance to e.g. antibiotics like ampicillin, kanamycin, chloramphenicol, erythromycin, tetracycline, spectinomycin, neomycin, hygromycin, methotrexate, or resistance to heavy metals, virus or herbicides, or which provides for prototrophy or auxotrophs. Examples of bacterial selectable markers are the *dal* genes from *Bacillus subtilis* or *Bacillus licheniformis*, resistance. A frequently used mammalian marker is the dihydrofolate reductase gene (DHFR). Suitable markers for yeast host cells are ADE2, HIS3, LEU2, LYS2, MET3, TRP1, and URA3. A selectable marker for use in a filamentous fungal host cell may be selected from the group including, but not limited to, *amdS* (acetamidase), *argB* (ornithine carbamoyltransferase), *bar* (phosphinothricin acetyltransferase), *hygB* (hygromycin phosphotransferase), *niaD* (nitrate reductase), *pyrG* (orotidine-5'-phosphate decarboxylase), *sC* (sulfate adenylyltransferase), *trpC* (anthranilate synthase), and glufosinate resistance markers, as well as equivalents from other species. Particularly, for use in an *Aspergillus* cell are the *amdS* and *pyrG* markers of *Aspergillus nidulans* or *Aspergillus oryzae* and the *bar* marker of *Streptomyces hygroscopicus*. Furthermore, selection may be accomplished by co-transformation, e.g., as described in WO 91/17243, where the selectable marker is on a separate vector.

To direct a subtilase variant of the present invention into the secretory pathway of the host cells, a secretory signal sequence (also known as a leader sequence, prepro sequence or pre sequence) may be provided in the recombinant vector. The secretory signal sequence is joined to the DNA sequence encoding the enzyme in the correct reading frame. Secretory signal sequences are commonly positioned 5' to the DNA sequence encoding the enzyme. The secretory signal sequence may be that normally associated with the enzyme or may be from a gene encoding another secreted protein.

The procedures used to ligate the DNA sequences coding for the present enzyme, the promoter and optionally the terminator and/or secretory signal sequence, respectively, or to assemble these sequences by suitable PCR amplification schemes, and to insert them into suitable vectors containing the information necessary for replication or integration, are well known to persons skilled in the art (cf., for instance, Sambrook et al.).

More than one copy of a nucleic acid sequence encoding an enzyme of the present invention may be inserted into the host cell to amplify expression of the nucleic acid sequence. Stable amplification of the nucleic acid sequence can be obtained by integrating at least one additional copy of the sequence into the host cell genome using methods well known in the art and selecting for transformants.

The nucleic acid constructs of the present invention may also comprise one or more nucleic acid sequences which encode one or more factors that are advantageous in the expression of the polypeptide, e.g., an activator (e.g., a trans-acting factor), a chaperone, and a processing protease. Any factor that is functional in the host cell of choice may be used in the present invention. The nucleic acids encoding one or more of these factors are not necessarily in tandem with the nucleic acid sequence encoding the polypeptide.

Host cells

The DNA sequence encoding a subtilase variant of the present invention may be either homologous or heterologous to the host cell into which it is introduced. If homologous to the host cell, i.e. produced by the host cell in nature, it will typically be operably connected to another promoter sequence or, if applicable, another secretory signal sequence and/or terminator sequence than in its natural environment. The term "homologous" is intended to include a DNA sequence encoding an enzyme native to the host organism in question. The term "heterologous" is intended to include a DNA sequence not expressed by the host cell in nature. Thus, the DNA sequence may be from another organism, or it may be a synthetic sequence.

The host cell into which the DNA construct or the recombinant vector of the invention is introduced may be any cell that is capable of producing the present subtilase variants, such as prokaryotes, e.g. bacteria or eukaryotes, such as fungal cells, e.g. yeasts or filamentous fungi, insect cells, plant cells or mammalian cells.

Examples of bacterial host cells which, on cultivation, are capable of producing the subtilase variants of the invention are gram-positive bacteria such as strains of *Bacillus*, e.g. strains of *B. subtilis*, *B. licheniformis*, *B. lentus*, *B. brevis*, *B. stearothermophilus*, *B. alkalophilus*, *B. amyloliquefaciens*, *B. coagulans*, *B. circulans*, *B. lautus*, *B. megaterium* or *B. thuringiensis*, or strains of *Streptomyces*, such as *S. lividans* or *S. murinus*, or gram-negative bacteria such as *Escherichia coli* or *Pseudomonas sp.*

The transformation of the bacteria may be effected by protoplast transformation, electroporation, conjugation, or by using competent cells in a manner known per se (cf. Sambrook et al., supra).

When expressing the subtilase variant in bacteria such as *E. coli*, the enzyme may be retained in the cytoplasm, typically as insoluble granules (known as inclusion bodies), or it may be directed to the periplasmic space by a bacterial secretion sequence. In the former case, the cells are lysed and the granules are recovered and denatured after which the enzyme is refolded by diluting the denaturing agent. In the latter case, the enzyme may be

recovered from the periplasmic space by disrupting the cells, e.g. by sonication or osmotic shock, to release the contents of the periplasmic space and recovering the enzyme.

When expressing the subtilase variant in gram-positive bacteria such as *Bacillus* or *Streptomyces* strains, the enzyme may be retained in the cytoplasm, or it may be directed to the extracellular medium by a bacterial secretion sequence. In the latter case, the enzyme may be recovered from the medium as described below.

Examples of host yeast cells include cells of a species of *Candida*, *Kluyveromyces*, *Saccharomyces*, *Schizosaccharomyces*, *Pichia*, *Hansehula*, or *Yarrowia*. In a particular embodiment, the yeast host cell is a *Saccharomyces carlsbergensis*, *Saccharomyces cerevisiae*, *Saccharomyces diastaticus*, *Saccharomyces douglasii*, *Saccharomyces kluyveri*, *Saccharomyces norbensis* or *Saccharomyces oviformis* cell. Other useful yeast host cells are a *Kluyveromyces lactis*, *Kluyveromyces fragilis*, *Hansehula polymorpha*, *Pichia pastoris*, *Yarrowia lipolytica*, *Schizosaccharomyces pombe*, *Ustilgo maylis*, *Candida maltose*, *Pichia guilliermondii* and *Pichia methanolio* cell (cf. Gleeson et al., J. Gen. Microbiol. 132, 1986, pp. 3459-3465; US 4,882,279 and US 4,879,231). Since the classification of yeast may change in the future, for the purposes of this invention, yeast shall be defined as described in Biology and Activities of Yeast (Skinner, F.A., Passmore, S.M., and Davenport, R.R., eds, Soc. App. Bacteriol. Symposium Series No. 9, 1980. The biology of yeast and manipulation of yeast genetics are well known in the art (see, e.g., Biochemistry and Genetics of Yeast, Bacil, M., Horecker, B.J., and Stopani, A.O.M., editors, 2nd edition, 1987; The Yeasts, Rose, A.H., and Harrison, J.S., editors, 2nd edition, 1987; and The Molecular Biology of the Yeast *Saccharomyces*, Strathern et al., editors, 1981). Yeast may be transformed using the procedures described by Becker and Guarente, In Abelson, J.N. and Simon, M.I., editors, Guide to Yeast Genetics and Molecular Biology, Methods in Enzymology, Volume 194, pp 182-187, Academic Press, Inc., New York; Ito et al., 1983, Journal of Bacteriology 153:163; and Hinnen et al., 1978, Proceedings of the National Academy of Sciences USA 75:1920.

Examples of filamentous fungal cells include filamentous forms of the subdivision Eumycota and Oomycota (as defined by Hawksworth et al., 1995, supra), in particular it may of the a cell of a species of *Acremonium*, such as *A. chrysogenum*, *Aspergillus*, such as *A. awamori*, *A. foetidus*, *A. japonicus*, *A. niger*, *A. nidulans* or *A. oryzae*, *Fusarium*, such as *F. batridioides*, *F. cerealis*, *F. crookwellense*, *F. culmorum*, *F. graminearum*, *F. graminum*, *F. heterosporum*, *F. negundi*, *F. reticulatum*, *F. roseum*, *F. sambucinum*, *F. sarcochroum*, *F. sulphureum*, *F. trichothecioides* or *F. oxysporum*, *Humicola*, such as *H. insolens* or *H. lanuginosa*, *Mucor*, such as *M. miehei*, *Myceliophthora*, such as *M. thermophilum*, *Neuro-*

spora, such as *N. crassa*, *Penicillium*, such as *P. purpurogenum*, *Thielavia*, such as *T. terrestris*, *Tolypocladium*, or *Trichoderma*, such as *T. harzianum*, *T. koningii*, *T. longibrachiatum*, *T. reesei* or *T. viride*, or a teleomorph or synonym thereof. The use of *Aspergillus* spp. for the expression of proteins is described in, e.g., EP 272 277, EP 230 023.

- 5 Examples of insect cells include a *Lepidoptera* cell line, such as *Spodoptera frugiperda* cells or *Trichoplusia ni* cells (cf. US 5,077,214). Culture conditions may suitably be as described in WO 89/01029 or WO 89/01028. Transformation of insect cells and production of heterologous polypeptides therein may be performed as described in US 4,745,051; US 4,775, 624; US 4,879,236; US 5,155,037; US 5,162,222; EP 397,485).
- 10 Examples of mammalian cells include Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, COS cells, or any number of other immortalized cell lines available, e.g., from the American Type Culture Collection. Methods of transfecting mammalian cells and expressing DNA sequences introduced in the cells are described in e.g. Kaufman and Sharp, J. Mol. Biol. 159 (1982), 601 - 621; Southern and Berg, J. Mol. Appl.
- 15 Genet. 1 (1982), 327 - 341; Loyter et al., Proc. Natl. Acad. Sci. USA 79 (1982), 422 - 426; Wigler et al., Cell 14 (1978), 725; Corsaro and Pearson, Somatic Cell Genetics 7 (1981), 603, Ausubel et al., Current Protocols in Molecular Biology, John Wiley and Sons, Inc., N.Y., 1987, Hawley-Nelson et al., Focus 15 (1993), 73; Ciccarone et al., Focus 15 (1993), 80; Graham and van der Eb, Virology 52 (1973), 456; and Neumann et al., EMBO J. 1
- 20 (1982), 841 - 845. Mammalian cells may be transfected by direct uptake using the calcium phosphate precipitation method of Graham and Van der Eb (1978, Virology 52:546).

Methods for expression and isolation of proteins

- 25 To express an enzyme of the present invention the above mentioned host cells transformed or transfected with a vector comprising a nucleic acid sequence encoding an enzyme of the present invention are typically cultured in a suitable nutrient medium under conditions permitting the production of the desired molecules, after which these are recovered from the cells, or the culture broth.

- The medium used to culture the host cells may be any conventional medium suitable for
- 30 growing the host cells, such as minimal or complex media containing appropriate supplements. Suitable media are available from commercial suppliers or may be prepared according to published recipes (e.g. in catalogues of the American Type Culture Collection). The media may be prepared using procedures known in the art (see, e.g., references for bacteria and yeast; Bennett, J.W. and LaSure, L., editors, More Gene Manipulations in Fungi,
- 35 Academic Press, CA, 1991).

If the enzymes of the present invention are secreted into the nutrient medium, they may be recovered directly from the medium. If they are not secreted, they may be recovered from cell lysates. The enzymes of the present invention may be recovered from the culture medium by conventional procedures including separating the host cells from the medium by centrifugation or filtration, precipitating the proteinaceous components of the supernatant or filtrate by means of a salt, e.g. ammonium sulphate, purification by a variety of chromatographic procedures, e.g. ion exchange chromatography, gelfiltration chromatography, affinity chromatography, or the like, dependent on the enzyme in question.

The enzymes of the invention may be detected using methods known in the art that are specific for these proteins. These detection methods include use of specific antibodies, formation of a product, or disappearance of a substrate. For example, an enzyme assay may be used to determine the activity of the molecule. Procedures for determining various kinds of activity are known in the art.

The enzymes of the present invention may be purified by a variety of procedures known in the art including, but not limited to, chromatography (e.g., ion exchange, affinity, hydrophobic, chromatofocusing, and size exclusion), electrophoretic procedures (e.g., preparative isoelectric focusing (IEF), differential solubility (e.g., ammonium sulfate precipitation), or extraction (see, e.g., Protein Purification, J-C Janson and Lars Ryden, editors, VCH Publishers, New York, 1989).

When an expression vector comprising a DNA sequence encoding an enzyme of the present invention is transformed/transfected into a heterologous host cell it is possible to enable heterologous recombinant production of the enzyme. An advantage of using a heterologous host cell is that it is possible to make a highly purified enzyme composition, characterized in being free from homologous impurities, which are often present when a protein or peptide is expressed in a homologous host cell. In this context homologous impurities mean any impurity (e.g. other polypeptides than the enzyme of the invention) which originates from the homologous cell where the enzyme of the invention is originally obtained from.

DETERGENT APPLICATIONS

The enzyme of the invention may be added to and thus become a component of a detergent composition.

The detergent composition of the invention may for example be formulated as a hand or machine laundry detergent composition including a laundry additive composition suitable for pre-treatment of stained fabrics and a rinse added fabric softener composition, or be

formulated as a detergent composition for use in general household hard surface cleaning operations, or be formulated for hand or machine dishwashing operations.

In a specific aspect, the invention provides a detergent additive comprising the enzyme of the invention. The detergent additive as well as the detergent composition may comprise one or more other enzymes such as a protease, a lipase, a cutinase, an amylase, a carbohydrate, a cellulase, a pectinase, a mannanase, an arabinase, a galactanase, a xylanase, an oxidase, e.g., a laccase, and/or a peroxidase.

In general the properties of the chosen enzyme(s) should be compatible with the selected detergent, (i.e. pH-optimum, compatibility with other enzymatic and non-enzymatic ingredients, etc.), and the enzyme(s) should be present in effective amounts.

Proteases: Suitable proteases include those of animal, vegetable or microbial origin. Microbial origin is preferred. Chemically modified or protein engineered mutants are included. The protease may be a serine protease or a metallo protease, preferably an alkaline microbial protease or a trypsin-like protease. Examples of alkaline proteases are subtilisins, especially those derived from *Bacillus*, e.g., subtilisin Novo, subtilisin Carlsberg, subtilisin 309, subtilisin 147 and subtilisin 168 (described in WO 89/06279). Examples of trypsin-like proteases are trypsin (e.g. of porcine or bovine origin) and the *Fusarium* protease described in WO 89/06270 and WO 94/25583.

Examples of useful proteases are the variants described in WO 92/19729, WO 98/20115, WO 98/20116, and WO 98/34946, especially the variants with substitutions in one or more of the following positions: 27, 36, 57, 76, 87, 97, 101, 104, 120, 123, 167, 170, 194, 206, 218, 222, 224, 235 and 274.

Preferred commercially available protease enzymes include Alcalase™, Savinase™, Primase™, Duralase™, Esperase™, and Kannase™ (Novo Nordisk A/S), Maxatase™, Maxacal™, Maxapem™, Properase™, Purafect™, Purafect OxP™, FN2™, and FN3™ (Genencor International Inc.).

Lipases: Suitable lipases include those of bacterial or fungal origin. Chemically modified or protein engineered mutants are included. Examples of useful lipases include lipases from *Humicola* (synonym *Thermomyces*), e.g. from *H. lanuginosa* (*T. lanuginosus*) as described in EP 258 068 and EP 305 216 or from *H. insolens* as described in WO 96/13580, a *Pseudomonas* lipase, e.g. from *P. alcaligenes* or *P. pseudoalcaligenes* (EP 218 272), *P. cepacia* (EP 331 376), *P. stutzeri* (GB 1,372,034), *P. fluorescens*, *Pseudomonas* sp. strain SD 705 (WO 95/06720 and WO 96/27002), *P. wisconsinensis* (WO 96/12012), a *Bacillus*

lipase, e.g. from *B. subtilis* (Dartois et al. (1993), Biochimica et Biophysica Acta, 1131, 253-360), *B. stearothermophilus* (JP 64/744992) or *B. pumilus* (WO 91/16422).

Other examples are lipase variants such as those described in WO 92/05249, WO 94/01541, EP 407 225, EP 260 105, WO 95/35381, WO 96/00292, WO 95/30744, WO 94/25578, WO 95/14783, WO 95/22615, WO 97/04079 and WO 97/07202.

Preferred commercially available lipase enzymes include Lipolase™ and Lipolase Ultra™ (Novo Nordisk A/S).

Amylases: Suitable amylases (α and/or β) include those of bacterial or fungal origin.

Chemically modified or protein engineered mutants are included. Amylases include, for example, α -amylases obtained from *Bacillus*, e.g. a special strain of *B. licheniformis*, described in more detail in GB 1,296,839.

Examples of useful amylases are the variants described in WO 94/02597, WO 94/18314, WO 96/23873, and WO 97/43424, especially the variants with substitutions in one or more of the following positions: 15, 23, 105, 106, 124, 128, 133, 154, 156, 181, 188, 190, 197, 202, 208, 209, 243, 264, 304, 305, 391, 408, and 444.

Commercially available amylases are Duramyl™, Termamyl™, Fungamyl™ and BAN™ (Novo Nordisk A/S), Rapidase™ and Purastar™ (from Genencor International Inc.).

Cellulases: Suitable cellulases include those of bacterial or fungal origin. Chemically modified or protein engineered mutants are included. Suitable cellulases include cellulases from the genera *Bacillus*, *Pseudomonas*, *Humicola*, *Fusarium*, *Thielavia*, *Acremonium*, e.g. the fungal cellulases produced from *Humicola insolens*, *Myceliophthora thermophila* and *Fusarium oxysporum* disclosed in US 4,435,307, US 5,648,263, US 5,691,178, US 5,776,757 and WO 89/09259.

Especially suitable cellulases are the alkaline or neutral cellulases having colour care benefits. Examples of such cellulases are cellulases described in EP 0 495 257, EP 0 531 372, WO 96/11262, WO 96/29397, WO 98/08940. Other examples are cellulase variants such as those described in WO 94/07998, EP 0 531 315, US 5,457,046, US 5,686,593, US 5,763,254, WO 95/24471, WO 98/12307 and PCT/DK98/00299.

Commercially available cellulases include Celluzyme™, and Carezyme™ (Novo Nordisk A/S), Clazinase™, and Puradax HA™ (Genencor International Inc.), and KAC-500(B)™ (Kao Corporation).

Peroxidases/Oxidases: Suitable peroxidases/oxidases include those of plant, bacterial or fungal origin. Chemically modified or protein engineered mutants are included. Examples of useful peroxidases include peroxidases from *Coprinus*, e.g. from *C. cinereus*, and variants thereof as those described in WO 93/24618, WO 95/10602, and WO 98/15257.

- 5 Commercially available peroxidases include Guardzyme™ (Novo Nordisk A/S).

The detergent enzyme(s) may be included in a detergent composition by adding separate additives containing one or more enzymes, or by adding a combined additive comprising all of these enzymes. A detergent additive of the invention, i.e. a separate additive or a combined additive, can be formulated e.g. as a granulate, a liquid, a slurry, etc. Preferred detergent additive formulations are granulates, in particular non-dusting granulates, liquids, in particular stabilized liquids, or slurries.

Non-dusting granulates may be produced, e.g., as disclosed in US 4,106,991 and 4,661,452 and may optionally be coated by methods known in the art. Examples of waxy coating materials are poly(ethylene oxide) products (polyethyleneglycol, PEG) with mean molar weights of 1000 to 20000; ethoxylated nonylphenols having from 16 to 50 ethylene oxide units; ethoxylated fatty alcohols in which the alcohol contains from 12 to 20 carbon atoms and in which there are 15 to 80 ethylene oxide units; fatty alcohols; fatty acids; and mono- and di- and triglycerides of fatty acids. Examples of film-forming coating materials suitable for application by fluid bed techniques are given in GB 1483591. Liquid enzyme preparations may, for instance, be stabilized by adding a polyol such as propylene glycol, a sugar or sugar alcohol, lactic acid or boric acid according to established methods. Protected enzymes may be prepared according to the method disclosed in EP 238,216.

- 25 The detergent composition of the invention may be in any convenient form, e.g., a bar, a tablet, a powder, a granule, a paste or a liquid. A liquid detergent may be aqueous, typically containing up to 70 % water and 0-30 % organic solvent, or non-aqueous.

The detergent composition comprises one or more surfactants, which may be non-ionic including semi-polar and/or anionic and/or cationic and/or zwitterionic. The surfactants are typically present at a level of from 0.1% to 60% by weight.

When included therein the detergent will usually contain from about 1% to about 40% of an anionic surfactant such as linear alkylbenzenesulfonate, alpha-olefinsulfonate, alkyl sulfate (fatty alcohol sulfate), alcohol ethoxysulfate, secondary alkanesulfonate, alpha-sulfo fatty acid methyl ester, alkyl- or alkenylsuccinic acid or soap.

When included therein the detergent will usually contain from about 0.2% to about 40% of a non-ionic surfactant such as alcohol ethoxylate, nonylphenol ethoxylate, alkylpolyglycoside, alkyldimethylamineoxide, ethoxylated fatty acid monoethanolamide, fatty acid monoethanolamide, polyhydroxy alkyl fatty acid amide, or N-acyl N-alkyl derivatives of glucosamine ("glucamides").

The detergent may contain 0-65 % of a detergent builder or complexing agent such as zeolite, diphosphate, triphosphate, phosphonate, carbonate, citrate, nitrilotriacetic acid, ethylenediaminetetraacetic acid, diethylenetriaminepentaacetic acid, alkyl- or alkenylsuccinic acid, soluble silicates or layered silicates (e.g. SKS-6 from Hoechst).

The detergent may comprise one or more polymers. Examples are carboxymethylcellulose, poly(vinylpyrrolidone), poly (ethylene glycol), poly(vinyl alcohol), poly(vinylpyridine-N-oxide), poly(vinylimidazole), polycarboxylates such as polyacrylates, maleic/acrylic acid copolymers and lauryl methacrylate/acrylic acid copolymers.

The detergent may contain a bleaching system which may comprise a H_2O_2 source such as perborate or percarbonate which may be combined with a peracid-forming bleach activator such as tetraacetythylenediamine or nonanoyloxybenzenesulfonate. Alternatively, the bleaching system may comprise peroxyacids of e.g. the amide, imide, or sulfone type.

The enzyme(s) of the detergent composition of the invention may be stabilized using conventional stabilizing agents, e.g., a polyol such as propylene glycol or glycerol, a sugar or sugar alcohol, lactic acid, boric acid, or a boric acid derivative, e.g., an aromatic borate ester, or a phenyl boronic acid derivative such as 4-formylphenyl boronic acid, and the composition may be formulated as described in e.g. WO 92/19709 and WO 92/19708.

The detergent may also contain other conventional detergent ingredients such as e.g. fabric conditioners including clays, foam boosters, suds suppressors, anti-corrosion agents, soil-suspending agents, anti-soil redeposition agents, dyes, bactericides, optical brighteners, hydrotropes, tarnish inhibitors, or perfumes.

It is at present contemplated that in the detergent compositions any enzyme, in particular the enzyme of the invention, may be added in an amount corresponding to 0.01-100 mg of

enzyme protein per liter of wash liquor, preferably 0.05-5 mg of enzyme protein per liter of wash liquor, in particular 0.1-1 mg of enzyme protein per liter of wash liquor.

The enzyme of the invention may additionally be incorporated in the detergent formulations disclosed in WO 97/07202 which is hereby incorporated as reference.

5

MATERIALS AND METHODS

Textiles

Standard textile pieces are obtained from EMPA St. Gallen, Lerchfeldstrasse 5, CH-9014
10 St. Gallen, Switzerland. Especially type EMPA 116 (cotton textile stained with blood, milk and ink) and EMPA 117 (polyester/cotton textile stained with blood, milk and ink).

Method for producing a subtilase variant

The present invention provides a method of producing an isolated enzyme according to the
15 invention, wherein a suitable host cell, which has been transformed with a DNA sequence encoding the enzyme, is cultured under conditions permitting the production of the enzyme, and the resulting enzyme is recovered from the culture.

When an expression vector comprising a DNA sequence encoding the enzyme is trans-
formed into a heterologous host cell it is possible to enable heterologous recombinant pro-
20 duction of the enzyme of the invention. Thereby it is possible to make a highly purified subtilase composition, characterized in being free from homologous impurities.

The medium used to culture the transformed host cells may be any conventional medium
suitable for growing the host cells in question. The expressed subtilase may conveniently
25 be secreted into the culture medium and may be recovered there-from by well-known procedures including separating the cells from the medium by centrifugation or filtration, precipitating proteinaceous components of the medium by means of a salt such as ammonium sulfate, followed by chromatographic procedures such as ion exchange chromatography, affinity chromatography, or the like.

30

EXAMPLE 1

Construction of library of Savinase variants

A library, based on Savinase positions V28, I35, T71, I72, A73, M175 and T224 (BPN'
numbering) have been synthesized. The library contains exclusively TY145-suggested al-
35 terations and covers the introduced mutations V28I,A,L; I35V,A,L; T71S; I72A,G,V;

A73L,G; M175V,A; T224S,A introduced in oligopeptides, some of which are doped. Doping of nucleotide bases from a desired doping of individual amino acid residues, which is used for the example below, can be calculated as described at page 18 herein.

In the attached sequence listing, the doped nucleotides below have been given the nucleotide symbols recommended by the WIPO Standard ST25.

The constructed oligopeptide primers are listed below. The primers are named after which positions are subject to modifications, thus 28-35-CN may have alterations in positions 28 and 35, 71-72-73-NC may have alterations in positions 71, 72 and 73, and so forth.

- 10 28-35-CN, SEQ ID NO:7
5'-TAG ATC TGG ATG AGT GGA (50%T/50%A)(80%A/10%G/10%C)(75%T/25%C) CCC
TGT ATC GAG GAC AGC (75%A/25%T)(90%A/10%G)(80%C/10%T/10%G) TTT TAC
ACC AGA ACC TGT-3'
- 15 28-35-NC, SEQ ID NO:8
5'-TCC ACT CAT CCA GAT CTA-3'
- (I) 71-72-73-CN, SEQ ID NO:9
20 5'-AAT CGA ATT GTT TAA AGC AGC (65%T/35%A)(80%A/10%C/10%G)(75%T/25%C)
(90%C/10%T)G(90%T/10%A) CCC GGC CAC ATG CGT GCC-3'
- (II) 71-72-73-CN, SEQ ID NO: 10
5'-AAT CGA ATT GTT TAA AGC AAG (65%T/35%A)(80%A/10%C/10%G)(75%T/25%C)
(90%C/10%T)G(90%T/10%A) CCC GGC CAC ATG CGT GCC-3'
- 25 (III) 71-72-73-CN, SEQ ID NO:11
5'-AAT CGA ATT GTT TAA AGC GCC (65%T/35%A)(80%A/10%C/10%G)(75%T/25%C)
(90%C/10%T)G(90%T/10%A) CCC GGC CAC ATG CGT GCC-3'
- 30 71-72-73-NC, SEQ ID NO: 12
5' GCT TTA AAC AAT TCG ATT 3'
- 139, SEQ ID NO:13
5'-GAT TAA CGC GTT GCC GCT TCT GCG-3'
- 35 (I) 175-CN (90%), SEQ ID NO:14
5'-ATC AGT AGC TCC GAC TGC CA(90%T/10%C) TGC GTT CGC ATA GCG CGC-3'
- (II) 175-CN (10%), SEQ ID NO:15
5'-ATC AGT AGC TCC GAC TGC CGC TGC GTT CGC ATA GCG CGC-3'
- 40 175-NC, SEQ ID NO:16
5'-GCA GTC GGA GCT ACT GAT-3'
- 224-CN, SEQ ID NO:17
45 5'-CGC ACC TGC AAC ATG AGG CG(80%T/10%C/10%A) AGC CAT CGA TGT ACC
GTT-3'
- 224-NC, SEQ ID NO:18

5'-CCT CAT GTT GCA GGT GCG-3'

317, SEQ ID NO:19

5'-TGG CGC AAT CGG TAC CAT GGG G-3'

5

The Savinase gene is used as template for five individual PCR reactions under standard PCR conditions (Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor, 1989) where the oligos are combined as follows:

317 with 28-35-CN, 28-35-NC with 71-72-73-CN (a mixture of 80% (I) 71-72-73-CN, 10% (II) 71-72-73-CN and 10% (III) 71-72-73-CN), 71-72-73-NC with 175-CN (a mixture of 90% (I) 175-CN and 10% (II) 175-CN), 175-NC with 224-CN, 224-NC with 139, giving PCR products of 125 bp, 126 bp, 312 bp, 165 bp and 158 bp respectively.

10 The library is assembled by an additional PCR reaction where the five PCR products are mixed in equal molar amounts. Thereby the library contains a large number of different Savinase variants altered in one or more of the mentioned positions. The PCR reaction was assembled using a PTC-200 DNA Engine (MJ Research, Watertown, MA) and the following cycling parameters: 1 cycle of 2 min at 94 °C followed by 25 cycles of 30 sec at 94 °C, 30 sec at 55 °C and 1 min at 68 °C, and 1 cycle of 2 min at 68 °C. The library was cloned by PCR multimerization (Shafikhani et al. 1997) into Savinase expression vector psx222 and transformed into a *B. subtilis* host for expression. Subsequently Savinase variants can be isolated from the library, purified and characterized.

20 Likewise, properties from a BPN' like subtilase could be transferred to TY145 like subtilase by applying a similar procedure.

25 **EXAMPLE 2**

Transfer of regions from TY145 to BPN' subtilases

The below mentioned highly mobile regions in TY145 have been selected for transfer from TY145 to Savinase. The Savinase regions (BPN' numbering) are deleted and the TY145 regions (SEQ ID NO:1) are inserted instead. In addition regions can be selected for transfer between the psychrophiles TA41/TA39 and BPN' type protease like Savinase, or from TA39/TA41 to TY145 type non-psychrophilic subtilases.

SEGMENT I

TY145 SAKDSLIIASAVD, positions 144-155
35 Savinase PSPSATLEQAVN, positions 129-140

SEGMENT II

TY145 AGNSGSGSNTIGFPGGLV, positions 168-185
 Savinase SGNSGAGSISYPARYA, positions 153-172

SEGMENT IV

5 TY145 ASVESTWYTGGYNTIS, positions 233-248
 Savinase VNVQSTYPGSTYASLN, positions 203-218

Savinase variants modified by receiving respectively segments II (Hybrid II), IV (Hybrid IV) or I+II (Hybrid I+II) from TY145 were observed to exhibit subtilase activity as determined by
 10 the formation of clearing zones on skim milk powder plates.

EXAMPLE 3

Transfer of regions from S39 to BPN' subtilases

The below mentioned highly mobile regions in the TA39 subtilase S39, determined by the
 15 previous described homology building programs, have been selected for transfer from S39 to Savinase. The Savinase regions (BPN' numbering) are deleted and the S39 regions (SEQ ID NO:2) are inserted instead. In addition regions can be selected for transfer between the psychrophiles TA41/TA39 and TY145 type non-psychrophilic subtilases. Savinase variant V104S is used as acceptor for the S39 segment II.

20

SEGMENT I

S39 MSLGSSG, positions 138-144
 Savinase LSLGSPS, positions 124-130

25 SEGMENT II

S39 MSLGSSGESSLI, positions 138-149
 Savinase variant V104S LSLGSPSPSATL, positions 124-135

Savinase variants modified by receiving respectively segments I or II from S39 were observed to have subtilase activity against the substrate suc-AAPF-pNA (Suc-Ala-Ala-Pro-Phe-pNA). The subtilase activity was determined in a temperature profile assay where specific activities i.e. micromole substrate per minute per mg enzyme against before mentioned substrates, were determined at every 5 degrees Celsius. The measurements were done in a Tris-base buffer pH 9.

35 To measure subtilase activity in suc-AAPF-pNA: 100 uL 1.56 mM Suc-Ala-Ala-Pro-Phe-pNA in 0.1 M Tris was added to 100 uL Tris-base, pH 9.0 buffer and 20 uL enzyme. The

development of the degradation product pNA (paranitrophenol) was measured as initial velocities at 405 nm on an Elisa Reader for 1 minute.

The Savinase variant with segment I substituted had less specific activity against suc-AAPF-pNA compared to Savinase, whereas the Savinase variant with segment II substituted had more than 2 times higher specific activity against suc-AAPF-pNA than Savinase. In an AMSA-test (performed like described in Example 5 herein) the wash performance was shown to be preserved in Savinase variant with segment II compared to Savinase.

EXAMPLE 4

Purification and assessment of enzyme concentration

After fermentation, purification of subtilisin variants is accomplished using Hydrophobic Charge Induction Chromatography (HCIC) and subsequent vacuum filtration.

To capture the enzyme, the HCIC uses a cellulose matrix to which 4-Mercapto-Ethyl-Pyridine (4-MEP) is bound.

Beads of the cellulose matrix sized 80-100 μm are mixed with a media containing yeast and the transformed *B. subtilis* capable of secreting the subtilisin variants and incubated at pH 9.5 in Unifilter[®] microplates.

As 4-MEP is hydrophobic at pH > 7 and the subtilisin variants are hydrophobic at pH 9.5 a hydrophobic association is made between the secreted enzyme and the 4-MEP on the beads. After incubation the media and cell debris is removed by vacuum filtration while the beads and enzyme are kept on the filter.

To elute the enzyme from the beads the pH is now lowered by washing the filter with an elution buffer (pH 5). Hereby the enzymes part from the beads and can be retrieved from the buffer.

The concentration of the purified subtilisin enzyme variants is assessed by active site titration (AST).

The purified enzyme is incubated with the high affinity inhibitor CI-2A at different concentrations to inhibit a varying amount of the active sites. The protease and inhibitor binds to each other at a 1:1 ratio and accordingly the enzyme concentration can be directly related to the concentration of inhibitor, at which all protease is inactive. To measure the residual protease activity, a substrate suc-AAPF-pNA (0.6 mM Suc-Ala-Ala-Pro-Phe-pNA in Tris/HCl buffer) is added after the incubation with inhibitor and during the following 4 min-

utes the development of the degradation product pNA (paranitrophenol) is measured periodically at 405 nm on an Elisa Reader.

EXAMPLE 5

5 Wash performance of detergent compositions comprising modified enzymes

Wash performance of detergent compositions comprising enzyme hybrids or enzyme variants of the present is tested at low washing temperature.

10 The Savinase variant Hybrid IV of Example 2 was tested for washing performance in two different assays; a microlitre scale assay (AMSA) and a millilitre scale assay (Mini wash).

AMSA

15 The enzyme variants of the present application were tested using the Automatic Mechanical Stress Assay (AMSA). With the AMSA test the wash performance of a large quantity of small volume enzyme-detergent solutions can be examined. The AMSA plate has a number of slots for test solutions and a lid firmly squeezing the textile swatch to be washed against all the slot openings. During the washing time, the plate, test solutions, textile and lid are vigorously shaken to bring the test solution in contact with the textile and apply mechanical stress. For further description see WO 02/42740 especially the
20 paragraph "Special method embodiments" at page 23-24.

The assay was conducted under the experimental conditions specified below:

Detergent base	Omo Acao
Detergent dosage	1.5 g/l
Test solution volume	160 micro l
pH	10-10.5 adjusted with NaHCO ₃
Wash time	12 minutes
Temperature	20°C
Water hardness	9°dH
Enzyme concentration in test solution	5 nM, 10 nM and 30 nM
Test material	EMPA 117

25 After washing the textile pieces were flushed in tap water and air-dried.

The performance of the enzyme variant is measured as the brightness of the colour of the

textile samples washed with that specific enzyme variant. Brightness can also be expressed as the intensity of the light reflected from the textile sample when luminated with white light. When the textile is stained the intensity of the reflected light is lower, than that of a clean textile. Therefore the intensity of the reflected light can be used to measure wash performance of an enzyme variant.

Colour measurements are made with a professional flatbed scanner (*PFU DL2400pro*), which is used to capture an image of the washed textile samples. The scans are made with a resolution of 200 dpi and with an output colour dept of 24 bits. In order to get accurate results, the scanner is frequently calibrated with a *Kodak reflective IT8 target*.

To extract a value for the light intensity from the scanned images, a special designed software application is used (*Novozymes Color Vector Analyzer*). The program retrieves the 24 bit pixel values from the image and converts them into values for red, green and blue (RGB). The intensity value (Int) is calculated by adding the RGB values together as vectors and then taking the length of the resulting vector:

$$Int = \sqrt{r^2 + g^2 + b^2}$$

The wash performance (P) of the variants was calculated in accordance with the below formula:

$$P = Int(v) - Int(r)$$

where

Int(v) is the light intensity value of textile surface washed with enzyme variant and

Int(r) is the light intensity value of textile surface washed with the reference enzyme subtilisin 309 (BLSAVI).

The result of the AMSA wash of Hybrid IV was a Performance Score of S (2) in accordance with the definition:

Performance Scores (S) are summing up the performances (P) of the tested enzyme variants as:

S (2) which indicates that the variant performs better than the reference at all three concentrations (5, 10 and 30 nM) and

S (1) which indicates that the variant performs better than the reference at one or two concentrations.

Mini wash assay

The millilitre scale wash performance assay was conducted under the following conditions:

Detergent base	Omo Acao detergent powder
Detergent dose	1.5 g/l
pH	"as is" in the current detergent solution and is not adjusted.
Wash time	14 min.
Temperature	20°C
Water hardness	9°dH, adjusted by adding $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$; $\text{MgCl}_2 \cdot 6\text{H}_2\text{O}$; NaHCO_3 ($\text{Ca}^{2+}:\text{Mg}^{2+}:\text{HCO}_3^- = 2:1:6$) to milli-Q water.
Enzymes	Hybrid IV, Savinase
Enzyme conc.	5 nM, 10 nM
Test system	125 ml glass beakers. Textile dipped in test solution. Continuously up and down, 50 times per minute
Textile/volume	1 textile piece (13 x 3 cm) in 50 ml test solution
Test material	EMPA 117 textile swatches

- 5 After wash the measurement of remission from the test material was done at 460 nm using a Zeiss MCS 521 VIS spectrophotometer. The measurements were done according to the manufacturer's protocol.

- 10 As shown in Table 1 the textile washed with the Savinase variant Hybrid IV at 20°C in Omo Acao has a higher remission than the textile washed with the parent. This result indicates that this variant has better wash performance at low temperature than the parent Savinase.

Table 1. Wash performance results of the subtilase variant in Omo Acao for a dosage of 5 nM and 10 nM enzyme.

Enzyme	Remission, 5 nM enzyme	Remission, 10 nM enzyme
Blank (no enzyme)	12,0	12,3
Savinase	15,8	17,4
Hybrid IV	17,0	18,3

15

As it can be concluded from Table 2 the modified subtilases of the invention exhibits an improvement in wash performance.

CLAIMS

1. A TY145 like subtilase which is at least 63% homologous to the sequence of SEQ ID NO:1, comprising the overall subtilisin fold and the following structural characteristics:

a) a twisted beta-sheet with 7 strands,

b) six alpha helices,

c) at least three ion-binding sites,

wherein the Strong ion-binding site of the BPN' like subtilases is not present, and with the exception of the TY145 subtilase, the S39 subtilase from TA39, the S41 subtilase from TA41, and sphericase from *B. sphaericus*.

2. The subtilase of claim 1, wherein the positions of said three ion-binding sites in the three-dimensional structure of the subtilase is defined by the distance to the c-alpha atoms of the three active site amino acid residues of the subtilases, that is Ser, His and Asp, and the c-alpha atom of the amino acid residue next to the active site Ser residue (next to Ser),

wherein said distances between:

a) the Weak ion-binding site and i) Asp c-alpha atom is 17.50-19.50Å, ii) His c-alpha atom is 21-23Å, iii) Ser c-alpha atom is 13.80-15.80Å, iv) next to Ser c-alpha atom is 15.80-17.80Å,

b) the Far ion-binding site and i) Asp c-alpha atom is 28.70-30.70Å, ii) His c-alpha atom is 28-30Å, iii) Ser c-alpha atom is 20-22Å, iv) next to Ser c-alpha atom is 19.50-21.50Å,

c) the Near ion-binding site and i) Asp c-alpha atom is 27-29Å, ii) His c-alpha atom is 29.50-31.50Å, iii) Ser c-alpha atom is 21.40-23.40Å, iv) next to Ser c-alpha atom is 22.50-24.50Å,

3. A subtilase according to claim 2 wherein the positions of the three ion-binding sites are defined by the distance to the c-alpha atoms of amino acid residues D35, H72, S251 and M252 of SEQ ID NO:1 or by the distances to the c-alpha atoms of equivalent amino acid residues in another subtilase of the invention in accordance with claim 1, wherein the distance between

a) the Weak ion-binding site and i) D35 c-alpha atom is 18.55Å, ii) H72 c-alpha atom is 21.98Å, iii) S251 c-alpha atom is 14.71Å, iv) M252 c-alpha atom is 16.75Å,

b) the Far ion-binding site and i) D35 c-alpha atom is 29.68Å, ii) H72 c-alpha atom is 29.10Å, iii) S251 c-alpha atom is 20.96Å, iv) M252 c-alpha atom is 20.35Å,

c) the Near ion-binding site and i) D35 c-alpha atom is 28.04Å, ii) H72 c-alpha atom is 30.43Å, iii) S251 c-alpha atom is 22.28Å, iv) M252 c-alpha atom is 23.58Å,

and wherein the variation on the above mentioned distances are $\pm 0.8\text{\AA}$, preferably $\pm 0.7\text{\AA}$, more preferably $\pm 0.6\text{\AA}$, more preferably $\pm 0.5\text{\AA}$, more preferably $\pm 0.4\text{\AA}$, or most preferably $\pm 0.3\text{\AA}$.

5 4. A method of producing a variant of a parent TY145 like subtilase, the variant having at least one altered property as compared to the parent TY145 like subtilase, the method comprising:

- a) modelling the parent TY145 like subtilase on the three-dimensional structure of a TY145 subtilase to produce a three-dimensional structure of the parent TY145 like subtilase;
10
- b) identifying on the basis of the comparison in step a) at least one structural part of the parent TY145 subtilase, wherein an alteration in said structural part is predicted to result in an altered property;
- c) modifying the nucleic acid sequence encoding the parent TY145 subtilase to produce a
15 nucleic acid sequence encoding deletion or substitution of one or more amino acids at a position corresponding to said structural part, or an insertion of one or more amino acid residues in positions corresponding to said structural part;
- d) expressing the modified nucleic acid sequence in a host cell to produce the variant TY145 subtilase;
- 20 e) isolating the produced subtilase;
- f) purifying the isolated subtilase and
- g) recovering the purified subtilase.

25 5. A method according to claim 4, wherein the TY145 subtilase on which the parent TY145 subtilase is modelled in step a) is at least 63% homologous to SEQ ID NO:1, preferably at least 65% homologous, more preferably at least 70%, more preferably at least 74%, more preferably at least 80%, more preferably at least 83%, more preferably at least 90%, more preferably at least 91%, more preferably at least 92%, more preferably at least 93%, more preferably at least 94%, more preferably at least 95%, more preferably at least 96%, more
30 preferably at least 97%, more preferably at least 98% or even more preferably at least 99% homologous to the sequence of SEQ ID NO:1.

6. A method according to claim 4 or 5, wherein the TY145 subtilase on which the parent TY145 subtilase is modelled in step a) is defined in accordance with claim 3.

7. A method of producing a variant of a parent Subtilisin family subtilase, the variant having at least one altered property as compared to the parent Subtilisin family subtilase, the method comprising:

- a) modelling the parent Subtilisin family subtilase on the three-dimensional structure of a Subtilisin family subtilase to produce a three-dimensional structure of the parent Subtilisin family subtilase;
- b) comparing the three-dimensional structure obtained in step a) to the three-dimensional structure of a TY145 like subtilase;
- c) identifying on the basis of the comparison in step b) at least one structural part of the parent Subtilisin family subtilase, wherein an alteration in said structural part is predicted to result in an altered property;
- d) modifying the nucleic acid sequence encoding the parent Subtilisin family subtilase to produce a nucleic acid sequence encoding deletion or substitution of one or more amino acids at a position corresponding to said structural part, or an insertion of one or more amino acid residues in positions corresponding to said structural part;
- e) expressing the modified nucleic acid sequence in a host cell to produce the variant Subtilisin family subtilase,
- f) isolating the produced subtilase,
- g) purifying the isolated subtilase and
- h) recovering the purified subtilase.

8. A method according to claim 7, wherein the Subtilisin family subtilase on which the parent Subtilisin family subtilase is modelled in step a) is at least 61% homologous to SEQ ID NO:5, preferably at least 63% homologous, preferably at least 65% homologous, more preferably at least 70%, more preferably at least 74%, more preferably at least 80%, more preferably at least 83%, more preferably at least 90%, more preferably at least 91%, more preferably at least 92%, more preferably at least 93%, more preferably at least 94%, more preferably at least 95%, more preferably at least 96%, more preferably at least 97%, more preferably at least 98% or even more preferably at least 99% homologous to the sequence of SEQ ID NO:5.

9. A method according to any of claim 7 and 8, wherein the TY145 subtilase of step b) is defined in accordance with claim 3.

10. A method according to any of claims 7-9, wherein the TY145 subtilase in step b) is at least 63% homologous with the sequence of SEQ ID NO:1, preferably at least 65% homologous, more preferably at least 70%, more preferably at least 74%, more preferably at least 80%, more preferably at least 83%, more preferably at least 90%, more preferably at least 91%, more preferably at least 92%, more preferably at least 93%, more preferably at least 94%, more preferably at least 95%, more preferably at least 96%, more preferably at least 97%, more preferably at least 98% or even more preferably at least 99% homologous to the sequence of SEQ ID NO:1.
11. A method of producing a variant of a parent TY145 like subtilase, the variant having at least one altered property as compared to the parent TY145 like subtilase, the method comprising:
- a) modelling the parent TY145 like subtilase on the three-dimensional structure of a TY145 like subtilase to produce a three-dimensional structure of the parent TY145 like subtilase;
 - b) comparing the three-dimensional structure obtained in step a) to the three-dimensional structure of a Subtilisin family subtilase;
 - c) identifying on the basis of the comparison in step b) at least one structural part of the parent TY145 like subtilase, wherein an alteration in said structural part is predicted to result in an altered property;
 - d) modifying the nucleic acid sequence encoding the parent TY145 like subtilase to produce a nucleic acid sequence encoding deletion or substitution of one or more amino acids at a position corresponding to said structural part, or an insertion of one or more amino acid residues in positions corresponding to said structural part;
 - e) expressing the modified nucleic acid sequence in a host cell to produce the variant TY145 like subtilase;
 - f) isolating the produced subtilase;
 - g) purifying the isolated subtilase and
 - h) recovering the purified subtilase.
12. A method according to claim 11, wherein the Subtilisin family subtilase of step b) is at least 61% homologous to SEQ ID NO:5, preferably at least 63% homologous, preferably at least 65% homologous, more preferably at least 70%, more preferably at least 74%, more preferably at least 80%, more preferably at least 83%, more preferably at least 90%, more preferably at least 91%, more preferably at least 92%, more preferably at least 93%, more

preferably at least 94%, more preferably at least 95%, more preferably at least 96%, more preferably at least 97%, more preferably at least 98% or even more preferably at least 99% homologous to the sequence of SEQ ID NO:5.

5 13. A method according to any of claim 11 and 12, wherein the parent TY145 like subtilase is defined in accordance with claim 3.

14. A method according to any of claims 11-13, wherein the parent TY145 like subtilase is at least 63% homologous with the sequence of SEQ ID NO:1, preferably at least 65% ho-
10 mologous, more preferably at least 70%, more preferably at least 74%, more preferably at least 80%, more preferably at least 83%, more preferably at least 90%, more preferably at least 91%, more preferably at least 92%, more preferably at least 93%, more preferably at least 94%, more preferably at least 95%, more preferably at least 96%, more preferably at least 97%, more preferably at least 98% or even more preferably at least 99% homologous
15 to the sequence of SEQ ID NO:1.

15. A variant subtilase comprising an alteration in one or more positions located at a distance of not more than 10Å to one of the ion-binding sites of TY145, wherein the positions, as specified in SEQ ID NO:1, located at a distance of not more than 10Å to:

- 20 a) the Weak ion-binding site are: 154, 155, 158, 164, 165, 166, 167, 168, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 211, 220, 221, 222, 223, 224, 225, 226, 227, 228, 277, 281 and 305,
- b) the Near ion-binding site are: 185, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 277, 281, 299, 300, 301, 304, 305,
- 25 c) the Far ion-binding site are: 193, 198, 199, 201, 202, 204, 216, 217, 219, 226, 227, 228, 229, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306 and 307.

16. A subtilase variant according to claim 15 wherein the alterations are one or more of the
30 substitutions I220S,T,D,E; T215S,D,E; G298A,S,T,D,E; G296A,S,T,D,E; V185T,D,E; I221N,D,T,E.

17. A TY145 like subtilase variant comprising the introduction of a ion-binding site corresponding to the Strong ion-binding site of the Subtilisin family subtilases, wherein said variant
35 has a deletion of or in the region H83-G90 of SEQ ID NO:1 and subsequent insertion of

one or more amino acid residues, preferably insertion of the sequence LNNSIG between residues A82 and V91.

18. A TY145 like subtilase variant in which one or more ion-binding sites have been removed, wherein said variant comprises one or both of the alterations

- a) deletion of or in the region K290-D300 of SEQ ID NO:1 and subsequent insertion of one or more amino acid residues, preferably insertion between I289 and Y301 of the sequence GDS or DST, and preferably further comprising the substitution S303Y,
- b) deletion of or in the region N212-R224 of SEQ ID NO:1 and subsequent insertion of one or more amino acid residues, preferably insertion of a proline residue or an alanine residue between G211 and D225.

19. A Subtilisin family subtilase variant in which the Strong ion-binding site has been removed, wherein said variant comprises deletion of or in the region L75-G80 (BPN' numbering), or a corresponding region in another Subtilisin family subtilase, and subsequent insertion of one or more amino acid residues, preferably insertion of the sequence GGSNG of positions 84-88 of TY145 (SEQ ID NO:1) between A74 and V81, and preferably further comprising one or both of the substitutions L80Y and Q2A,N.

20. A TY145 like subtilase variant comprising one or more alterations in one or more of the positions contained in the following highly mobile regions:

84, 85, 86, 87 and 88,

108, 109, 110, 111, 112, 113, 114, 115, 116 and 117,

141, 142, 143, 144, 145 and 146,

150, 151 and 152,

169, 170 and 171,

200 and 201,

211, 212, 213, 214, 215, 216, 217, 218, 219 and 220,

242 and 243,

268, 269 and 270.

21. A TY145 like subtilase variant comprising one or more alterations in one or more of the positions contained in the following mobile regions:

1, 2, 3, 4, 5, 6 and 7,

17, 18, 19, 20, 21, 22 and 23,

38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 and 50,
 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68 and 69,
 84, 85, 86, 87, 88, 89, 90, 91 and 92,
 107, 108, 109 and 110,

5 239, 240, 241, 242 and 243
 265 and 266,

wherein said alterations preferably are introduced in one or both of the regions 57-69 and 84-92.

10 22. A TY145 like subtilase variant comprising one or more disulfide bridges introduced by one or more of the following modifications: G26C+A95C; A167C+T254C; R203C+G292C; V228C+A284C, wherein the positions corresponds to the positions in SEQ ID NO:1

23. A TY145 like subtilase variant comprising the substitution D116H,K,R.

15

24. A TY145 like subtilase variant comprising an alteration in one or more of the positions 18, 115, 185, 269 and 293 of SEQ ID NO:1, wherein the preferred alterations are Q18P, D115P, V185P, T269P and I293P.

20 25. A TY145 like subtilase variant comprising an alteration in one or more of the positions contained in the following regions:

16, 17, 18, 19, 20, 21 and 22,

40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63,
 64, 65, 66, 67, 68, 69, 70, 71, 72 and 73,

25 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130 and 131,

140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156,
 157, 158, 159, 160 and 161,

275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292,
 293 and 294,

30 wherein such alterations preferably are made in one or both the regions 40-73 and 140-161, preferably in the sub-regions 65-73 and 140-150.

26. A BPN' like subtilase variant comprising one or more of the alterations V28I,A,L; I35V,A,L; T71S; I72A,G,V; A73L,G; M175V,A; and T224S,A, wherein preferred variants of

Savinase comprises one or more of the substitutions V28I, I35V, T71S, I72A, A73L, M175V and T224S (BPN' numbering).

27. A TY145 like subtilase variant comprising an alteration in one or more of the following
 5 positions: 35,36,70,72,106,109,110,111,112,113,114,117,139,140,141,142,143,144,145,
 147,150,167,168,169,170,171,172,173,174,177,180,207,239,247,148,149,150,151 and
 252 of SEQ ID NO:1.

28. A BPN' like subtilase variant comprising one or more of the following alterations:

- 10 a) deletion of residues PSPSATLEQAVN (positions 129-140) in Savinase (BPN' numbering) and subsequent insertion of residues SAKDSLIASAVD (positions 144-155) from TY145 between S128 and S141 in Savinase,
- b) deletion of residues SGNSGAGSISYPARYA (positions 153-172) in Savinase (BPN' numbering) and subsequent insertion of residues AGNSGSGSNTIGFPGGLV (posi-
 15 tions 168-185) from TY145 between A152 and N173 in Savinase,
- c) deletion of residues VNVQSTYPGSTYASLN (positions 203-218) in Savinase (BPN' numbering) and subsequent insertion of residues ASVESTWYTGGYNTIS (positions 233-248) from TY145 between G202 and G219 in Savinase.

20 29. A TY145 like subtilase variant comprising an alteration in one or more of the following positions: V31, V38, T79, V80, L81, V188, T254, wherein preferred variants comprise one or more of V31I, T79S and V80A.

25 30. An isolated nucleic acid sequence comprising a nucleic acid sequence, which encodes for the subtilase variant defined or produced in any of the preceding claims.

31. An isolated nucleic acid sequence according to claim 30, wherein the nucleic acid sequence is selected from the group consisting of:

- 30 a) a nucleic acid sequence having at least 40% homology with the nucleic acid sequence shown in SEQ ID NO:20 or SEQ ID NO:21, and
- b) a nucleic acid sequence which hybridizes under low stringency conditions, preferably under medium stringency conditions, in particular under high stringency conditions, with
- c) a complementary strand of the nucleic acid sequence shown in SEQ ID NO:20 or SEQ
 35 ID NO:21, or

d) a subsequence of any of a), b) or c) of at least 100 nucleotides.

32. An isolated nucleic acid sequence according to claim 31, wherein the nucleic acid sequence has at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% homology with the nucleic acid sequence shown in SEQ ID NO:20 or SEQ ID NO:21.

33. An isolated nucleic acid construct comprising a nucleic acid sequence as defined in any of claims 30-32, operably linked to one or more control sequences capable of directing the expression of the polypeptide in a suitable expression host.

34. A recombinant host cell comprising the nucleic acid construct of claim 33.

35. A method for producing the variant defined in any of the preceding claims, the method comprising:

- a) cultivating the recombinant host cell of claim 34 under conditions conducive to the production of the subtilase variant; and
- b) recovering the variant.

36. A detergent composition comprising a TY145 like subtilase variant or a BPN' like subtilase variant.

37. Use of a TY145 like subtilase variant or a BPN' like subtilase variant in cleaning or washing applications.

38. A BPN' like subtilase variant comprising one or more of the following alterations:

- a) deletion of residues LSLGSPS (positions 124-130) in Savinase (BPN' numbering) and subsequent insertion of residues MSLGSSG (positions 248-254) from TA39 subtilase between N123 and P131 in Savinase,
- b) deletion of residues LSLGSPSPSATL (positions 124-135) in Savinase variant V104S (BPN' numbering) and subsequent insertion of residues MSLGSSGESSLI (positions 248-259) from TA39 subtilase between N123 and E136 in Savinase variant V104S.

ABSTRACT

The present invention relates to methods for producing variants of a parent TY145 subtilase and of a parent BPN' subtilase and to TY145 and BPN' variants having altered properties as compared to the parent TY145/BPN' subtilase.

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Figure 1.

5	RASQQIPWG	IKAIYNNDTL	TSTTGGSGIN	IAVLDTGVNT	SHPDLVNNVE	49	B.sphaericus
	AVPSTQTPWG	IKSIYNDQSI	TKTTGGSGIK	VAVLDTGVYT	SHLDLAGSAE	50	TY145
	MAASQSTPWG	IKAIYNNNSL	TSTSGGAGIN	IAVLDTGVNT	NHPDLSNNVE	50	TA41
	MAASQSTPWG	IKAIYNNSSI	TQTSGGGGIN	IAVLDTGVNT	NHPDLRNNVE	50	TA39
	AQSVPWG	ISRVQAPAAH	NRGLTGSGVK	VAVLDTGIS	THPDL NIR	46	Savinase
10	QCKDFTGATT	PINNSCTDRN	GHGTHVAGTA	LADGGSDQAG	IYGVAPDADL	99	
	QCKDFTQSNP	LVDGSCTDRQ	GHGTHVAGTV	LAHGGSNQOG	VYGVAPQAKL	100	
	QCKDFTVGTN	FTDNSCTDRQ	GHGTHVAGSA	LANGGT GSG	VYGVAPDADL	99	
	QCKDFTVGTG	YTNNSCTDRQ	GHGTHVAGSA	LADGGT GNG	VYGVAPDADL	99	
15	GGASFVPGEP	STQDGN	GHGTHVAGTI	AALNN SIG	VLGVAPSAEL	88	
	WAYKVLLDSG	SGYSDDIAAA	IRHAADQATA	TGTKTIISMS	LGSSANNSLI	149	
	WAYKVLGDNG	SGYSDDIAAA	IRHVADEASR	TGSKVVINMS	LGSSAKDSL	150	
	WAYKVLGDDG	SGYADDIAEA	IRHAGDQATA	LNTKVVINMS	LGSSGESSLI	149	
20	WAYKVLGDDG	SGYADDIAAA	IRHAGDQATA	LNTKVVINMS	LGSSGESSLI	149	
	YAVKVLGASG	SGSVSSIAQG	LEWAGNNG	MHVANLS	LGSPSPSATL	133	
	SSAVNYAYSK	GVLIVAAAGN	SGYSQGTIGY	PGALPNAIAV	AALENVQQNG	199	
	ASAVDYAYGK	GVLIVAAAGN	SGSGSNTIGF	PGGLVNAVAV	AALENVQQNG	200	
25	TNAVYAYDK	GVLIIAAAGN	SGPKPGSIGY	PGALVNAVAV	AALENTIQQNG	199	
	TNAVNYSYNK	GVLIIAAAGN	SGPYQGSIGY	PGALVNAVAV	AALENKVENG	199	
	EQAVNSATSR	GVLVVAASGN	SGA GSISY	PARYANAMAV	GATDQN	176	
	TYRVADYSSR	GYISTAGDYV	IQEGDIEISA	PGSSVYSTWY	NGGYNTISGT	249	
30	TYRVADFSSR	GNPATAGDYI	IQERDIEVSA	PGASVESTWY	TGGYNTISGT	250	
	TYRVADFSSR	GHKRTAGDYV	IQKGDVEISA	PGAAYYSTWF	DGGYATISGT	249	
	TYRVADFSSR	GYSWTDGDYA	IQKGDVEISA	PGAAIYSTWF	DGGYATISGT	249	
	NNRASFSQY	GA	GLDIVA	PGVNVQSTYP	GSTYASLNGT	214	
35	SMATPHVSGL	AAKIWAENPS	LSNTQLRSNL	QERAKSVDIK	GGYGAAIGDD	299	
	SMATPHVAGL	AAKIWSANTS	LSHSQRLTEL	QNRKAVYDIK	GGIGAGTGDD	300	
	SMASPHAAGL	AAKIWAQSPA	ASNVDVRGEL	QTRASVNDIL	SGNSAGSGDD	299	
	SMASPHAAGL	AAKIWAQYPS	ASNVDVRGEL	QYRAYENDIL	SGYYAGYGDD	299	
	SMATPHVAGA	AALVKQKNPS	WSNVQIRNHL	KNTA TSLG	ST	255	
40	YASGFGFARV	Q				310	
	YASGFGYPRV	K				311	
	IASGFGFAKV	Q				310	
	FASGFGFATV	Q				310	
45	NLYGSGLVNA	EAATR				269	

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Figure 2.

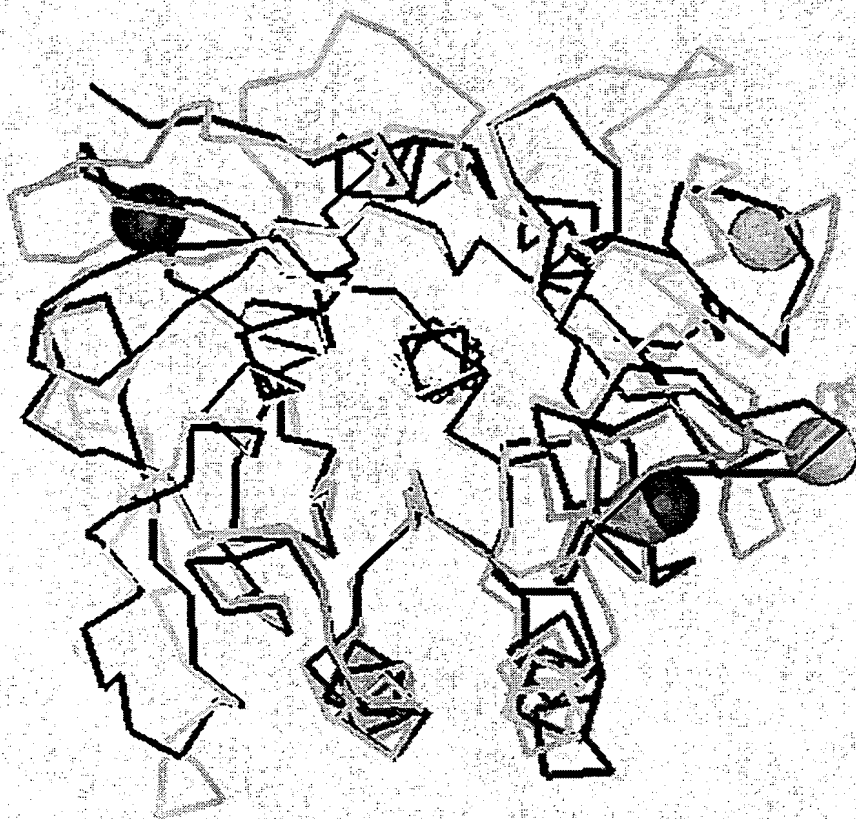
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1 BSTA41	100	93	76	51	50	51	55	52	54	58	58	59	57	60	60
2 BSTA39		100	75	52	52	52	56	53	55	58	58	61	58	62	61
3 TY145			100	60	60	60	58	60	62	58	57	59	59	62	59
4 BSAMY				100	99	99	97	91	76	63	69	74	66	74	74
5 BSSJ					100	99	97	90	76	69	74	66	74	74	56
6 BSNAT						100	98	91	77	63	69	74	66	74	74
7 BPMES							100	88	79	69	67	74	74	74	74
8 BPN'								100	77	66	71	74	67	74	74
9 BLSCAR									100	64	69	74	67	73	73
10 BHSAH										100	99	76	72	76	76
11 BLS147											100	76	76	76	76
12 BLSAVI												100	99	99	99
13 BAALKP													100	99	99
14 BSKSMK														100	98
15 BLSUBL															100

Figure 2, Matrix of homology between subtilases pertaining to the TY145 and BPN' subgroups.

The sequences are identified by sequence database accession numbers.

- 1: q45681; Subtilase derived from *B. subtilis* (BSTA41)
- 2: p28842; Psychrophilic subtilisin derived from Antarctic *Bacillus* strain (BSTA39)
- 3: abb77095; Subtilase derived from *Bacillus* sp. (TY145)
- 4: p00783; Subtilase derived from *Bacillus subtilis* var. *amylosacchariticus* (BSAMY)
- 5: p29142; Subtilase derived from *Bacillus stearothermophilus* (BSSJ)
- 6: p35835; Subtilase derived from *Bacillus subtilis* var. *natto*. (BSNAT)
- 7: p07518; Subtilase derived from *Bacillus pumilus* (*B. mesentericus*) (BPMES)
- 8: p00782; Subtilase derived from *Bacillus amyloliquefaciens* (BPN')
- 9: p00780; Subtilase derived from *Bacillus licheniformis* (BLSCAR)
- 10: p41363; Subtilase derived from *Bacillus halodurans* (BHSAH)
- 11: aaw62222; Subtilase derived from *Bacillus lentus* (BLS147)
- 12: p29600; Subtilase derived from *Bacillus lentus* (BLSAVI, BLS309)
- 13: p27693; Subtilase derived from *Bacillus alcalophilus* (BAALKP)
- 14: q99405; Subtilase derived from *Bacillus* sp. strain KSM-K16 (BSKSMK)
- 15: p29599; Subtilase derived from *Bacillus lentus* (BLSUBL).

Figure 3. Alignment of TY145 and BPN' structures, with indication of ion-binding sites. TY145 structure and ion-binding sites are yellow (light) and BPN' structure and ion-binding sites are blue (dark).



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SEQ list 10203.ST25
SEQUENCE LISTING

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<120> Subtilase variants

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Val Leu Asp Thr Gly Val Tyr Thr Ser His Leu Asp Leu Ala Gly Ser
35 40 45

Ala Glu Gln Cys Lys Asp Phe Thr Gln Ser Asn Pro Leu Val Asp Gly
50 55 60

Ser Cys Thr Asp Arg Gln Gly His Gly Thr His Val Ala Gly Thr Val
65 70 75 80

Leu Ala His Gly Gly Ser Asn Gly Gln Gly Val Tyr Gly Val Ala Pro
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Gln Ala Lys Leu Trp Ala Tyr Lys Val Leu Gly Asp Asn Gly Ser Gly
100 105 110

Tyr Ser Asp Asp Ile Ala Ala Ala Ile Arg His Val Ala Asp Glu Ala
115 120 125

Ser Arg Thr Gly Ser Lys Val Val Ile Asn Met Ser Leu Gly Ser Ser
130 135 140

Ala Lys Asp Ser Leu Ile Ala Ser Ala Val Asp Tyr Ala Tyr Gly Lys
145 150 155 160

Gly Val Leu Ile Val Ala Ala Ala Gly Asn Ser Gly Ser Gly Ser Asn
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Ser Arg Gly Asn Pro Ala Thr Ala Gly Asp Tyr Ile Ile Gln Glu Arg
 210 215 220

Asp Ile Glu Val Ser Ala Pro Gly Ala Ser Val Glu Ser Thr Trp Tyr
 225 230 235 240

Thr Gly Gly Tyr Asn Thr Ile Ser Gly Thr Ser Met Ala Thr Pro His
 245 250 255

Val Ala Gly Leu Ala Ala Lys Ile Trp Ser Ala Asn Thr Ser Leu Ser
 260 265 270

His Ser Gln Leu Arg Thr Glu Leu Gln Asn Arg Ala Lys Val Tyr Asp
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 35 40 45

Lys Asn Leu Lys Asn Ala Lys Gln Gln Tyr Gly Val His Trp Asp Phe
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Ala Gly Glu Gly Phe Thr Thr Asp Met Asn Glu Lys Gln Phe Asn Ala
 65 70 75 80

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85 90 95

Ile Ala Thr Ala Thr Asp Lys Pro Glu Ala Leu Tyr Asn Ala Met Ala
100 105 110

Ala Ser Gln Ser Thr Pro Trp Gly Ile Lys Ala Ile Tyr Asn Asn Ser
115 120 125

Ser Ile Thr Gln Thr Ser Gly Gly Gly Gly Ile Asn Ile Ala Val Leu
130 135 140

Asp Thr Gly Val Asn Thr Asn His Pro Asp Leu Arg Asn Asn Val Glu
145 150 155 160

Gln Cys Lys Asp Phe Thr Val Gly Thr Thr Tyr Thr Asn Asn Ser Cys
165 170 175

Thr Asp Arg Gln Gly His Gly Thr His Val Ala Gly Ser Ala Leu Ala
180 185 190

Asp Gly Gly Thr Gly Asn Gly Val Tyr Gly Val Ala Pro Asp Ala Asp
195 200 205

Leu Trp Ala Tyr Lys Val Leu Gly Asp Asp Gly Ser Gly Tyr Ala Asp
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Asp Ile Ala Ala Ala Ile Arg His Ala Gly Asp Gln Ala Thr Ala Leu
225 230 235 240

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245 250 255

Ser Leu Ile Thr Asn Ala Val Asn Tyr Ser Tyr Asn Lys Gly Val Leu
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Ile Ile Ala Ala Ala Gly Asn Ser Gly Pro Tyr Gln Gly Ser Ile Gly
275 280 285

Tyr Pro Gly Ala Leu Val Asn Ala Val Ala Val Ala Ala Leu Glu Asn
290 295 300

Lys Val Glu Asn Gly Thr Tyr Arg Val Ala Asp Phe Ser Ser Arg Gly
305 310 315 320

Tyr Ser Trp Thr Asp Gly Asp Tyr Ala Ile Gln Lys Gly Asp Val Glu
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SEQ list 10203.ST25

Tyr Ala Thr Ile Ser Gly Thr Ser Met Ala Ser Pro His Ala Ala Gly
355 360 365

Leu Ala Ala Lys Ile Trp Ala Gln Tyr Pro Ser Ala Ser Asn Val Asp
370 375 380

Val Arg Gly Glu Leu Gln Tyr Arg Ala Tyr Glu Asn Asp Ile Leu Ser
385 390 395 400

Gly Tyr Tyr Ala Gly Tyr Gly Asp Asp Phe Ala Ser Gly Phe Gly Phe
405 410 415

Ala Thr Val Gln
420

<210> 3
<211> 419
<212> PRT
<213> TA41 subtilase

<220>
<221> PEPTIDE
<222> (1)..(419)

<400> 3

Met Lys Arg Ser Gly Lys Ile Phe Thr Thr Ala Met Leu Ala Val Thr
1 5 10 15

Leu Met Met Pro Ala Ile Gly Val Ser Ala Asn Arg Gly Asn Ala Ala
20 25 30

Asp Gly Asn Glu Lys Phe Arg Val Leu Val Asp Ser Ala Asn Gln Asn
35 40 45

Asn Leu Lys Asn Val Lys Glu Gln Tyr Gly Val His Trp Asp Phe Ala
50 55 60

Gly Glu Gly Phe Thr Thr Asn Met Asn Glu Lys Gln Phe Asn Ala Leu
65 70 75 80

Gln Asn Asn Lys Asn Leu Thr Val Glu Lys Val Pro Glu Leu Glu Ile
85 90 95

Ala Thr Ala Thr Asn Lys Pro Glu Ala Leu Tyr Asn Ala Met Ala Ala
100 105 110

Ser Gln Ser Thr Pro Trp Gly Ile Lys Ala Ile Tyr Asn Asn Ser Asn
115 120 125

Leu Thr Ser Thr Ser Gly Gly Ala Gly Ile Asn Ile Ala Val Leu Asp
130 135 140

SEQ list 10203.ST25

Thr Gly Val Asn Thr Asn His Pro Asp Leu Ser Asn Asn Val Glu Gln
145 150 155 160

Cys Lys Asp Phe Thr Val Gly Thr Asn Phe Thr Asp Asn Ser Cys Thr
165 170 175

Asp Arg Gln Gly His Gly Thr His Val Ala Gly Ser Ala Leu Ala Asn
180 185 190

Gly Gly Thr Gly Ser Gly Val Tyr Gly Val Ala Pro Glu Ala Asp Leu
195 200 205

Trp Ala Tyr Lys Val Leu Gly Asp Asp Gly Ser Gly Tyr Ala Asp Asp
210 215 220

Ile Ala Glu Ala Ile Arg His Ala Gly Asp Gln Ala Thr Ala Leu Asn
225 230 235 240

Thr Lys Val Val Ile Asn Met Ser Leu Gly Ser Ser Gly Glu Ser Ser
245 250 255

Leu Ile Thr Asn Ala Val Asp Tyr Ala Tyr Asp Lys Gly Val Leu Ile
260 265 270

Ile Ala Ala Ala Gly Asn Ser Gly Pro Lys Pro Gly Ser Ile Gly Tyr
275 280 285

Pro Gly Ala Leu Val Asn Ala Val Ala Val Ala Ala Leu Glu Asn Thr
290 295 300

Ile Gln Asn Gly Thr Tyr Arg Val Ala Asp Phe Ser Ser Arg Gly His
305 310 315 320

Lys Arg Thr Ala Gly Asp Tyr Val Ile Gln Lys Gly Asp Val Glu Ile
325 330 335

Ser Ala Pro Gly Ala Ala Val Tyr Ser Thr Trp Phe Asp Gly Gly Tyr
340 345 350

Ala Thr Ile Ser Gly Thr Ser Met Ala Ser Pro His Ala Ala Gly Leu
355 360 365

Ala Ala Lys Ile Trp Ala Gln Ser Pro Ala Ala Ser Asn Val Asp Val
370 375 380

Arg Gly Glu Leu Gln Thr Arg Ala Ser Val Asn Asp Ile Leu Ser Gly
385 390 395 400

Asn Ser Ala Gly Ser Gly Asp Asp Ile Ala Ser Gly Phe Gly Phe Ala
405 410 415

SEQ list 10203.ST25

Lys val Gln

<210> 4
 <211> 310
 <212> PRT
 <213> B. sphaericus sphericase

<220>
 <221> PEPTIDE
 <222> (1)..(310)

<400> 4

Arg Ala Ser Gln Gln Ile Pro Trp Gly Ile Lys Ala Ile Tyr Asn Asn
 1 5 10 15

Asp Thr Leu Thr Ser Thr Thr Gly Gly Ser Gly Ile Asn Ile Ala Val
 20 25 30

Leu Asp Thr Gly Val Asn Thr Ser His Pro Asp Leu Val Asn Asn Val
 35 40 45

Glu Gln Cys Lys Asp Phe Thr Gly Ala Thr Thr Pro Ile Asn Asn Ser
 50 55 60

Cys Thr Asp Arg Asn Gly His Gly Thr His Val Ala Gly Thr Ala Leu
 65 70 75 80

Ala Asp Gly Gly Ser Asp Gln Ala Gly Ile Tyr Gly Val Ala Pro Asp
 85 90 95

Ala Asp Leu Trp Ala Tyr Lys Val Leu Leu Asp Ser Gly Ser Gly Tyr
 100 105 110

Ser Asp Asp Ile Ala Ala Ala Ile Arg His Ala Ala Asp Gln Ala Thr
 115 120 125

Ala Thr Gly Thr Lys Thr Ile Ile Ser Met Ser Leu Gly Ser Ser Ala
 130 135 140

Asn Asn Ser Leu Ile Ser Ser Ala Val Asn Tyr Ala Tyr Ser Lys Gly
 145 150 155 160

Val Leu Ile Val Ala Ala Ala Gly Asn Ser Gly Tyr Ser Gln Gly Thr
 165 170 175

Ile Gly Tyr Pro Gly Ala Leu Pro Asn Ala Ile Ala Val Ala Ala Leu
 180 185 190

Glu Asn Val Gln Gln Asn Gly Thr Tyr Arg Val Ala Asp Tyr Ser Ser
 195 200 205

SEQ list 10203.ST25

Arg Gly Tyr Ile Ser Thr Ala Gly Asp Tyr Val Ile Gln Glu Gly Asp
 210 215 220

Ile Glu Ile Ser Ala Pro Gly Ser Ser Val Tyr Ser Thr Trp Tyr Asn
 225 230 235 240

Gly Gly Tyr Asn Thr Ile Ser Gly Thr Ser Met Ala Thr Pro His Val
 245 250 255

Ser Gly Leu Ala Ala Lys Ile Trp Ala Glu Asn Pro Ser Leu Ser Asn
 260 265 270

Thr Gln Leu Arg Ser Asn Leu Gln Glu Arg Ala Lys Ser Val Asp Ile
 275 280 285

Lys Gly Gly Tyr Gly Ala Ala Ile Gly Asp Asp Tyr Ala Ser Gly Phe
 290 295 300

Gly Phe Ala Arg Val Gln
 305 310

<210> 5
 <211> 275
 <212> PRT
 <213> Bacillus amyloliquefaciens

<220>
 <221> PEPTIDE
 <222> (1)..(275)
 <223> BPN'

<400> 5

Ala Gln Ser Val Pro Tyr Gly Val Ser Gln Ile Lys Ala Pro Ala Leu
 1 5 10 15

His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp
 20 25 30

Ser Gly Ile Asp Ser Ser His Pro Asp Leu Lys Val Ala Gly Gly Ala
 35 40 45

Ser Met Val Pro Ser Glu Thr Asn Pro Phe Gln Asp Asn Asn Ser His
 50 55 60

Gly Thr His Val Ala Gly Thr Val Ala Ala Leu Asn Asn Ser Ile Gly
 65 70 75 80

Val Leu Gly Val Ala Pro Ser Ala Ser Leu Tyr Ala Val Lys Val Leu
 85 90 95

Gly Ala Asp Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu
 100 105 110

SEQ list 10203.ST25

Trp Ala Ile Ala Asn Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly
115 120 125

Pro Ser Gly Ser Ala Ala Leu Lys Ala Ala Val Asp Lys Ala Val Ala
130 135 140

Ser Gly Val Val Val Val Ala Ala Ala Gly Asn Glu Gly Thr Ser Gly
145 150 155 160

Ser Ser Ser Thr Val Gly Tyr Pro Gly Lys Tyr Pro Ser Val Ile Ala
165 170 175

Val Gly Ala Val Asp Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Val
180 185 190

Gly Pro Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr
195 200 205

Leu Pro Gly Asn Lys Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Ser
210 215 220

Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Asn
225 230 235 240

Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Glu Asn Thr Thr Thr Lys
245 250 255

Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala
260 265 270

Ala Ala Gln
275

<210> 6
<211> 269
<212> PRT
<213> Bacillus lentus

<220>
<221> PEPTIDE
<222> (1)..(269)
<223> Savinase

<400> 6

Ala Gln Ser Val Pro Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala
1 5 10 15

His Asn Arg Gly Leu Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp
20 25 30

Thr Gly Ile Ser Thr His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser
35 40 45

SEQ list 10203.ST25

Phe Val Pro Gly Glu Pro Ser Thr Gln Asp Gly Asn Gly His Gly Thr
50 55 60

His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu
65 70 75 80

Gly Val Ala Pro Ser Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala
85 90 95

Ser Gly Ser Gly Ser Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala
100 105 110

Gly Asn Asn Gly Met His Val Ala Asn Leu Ser Leu Gly Ser Pro Ser
115 120 125

Pro Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly
130 135 140

Val Leu Val Val Ala Ala Ser Gly Asn Ser Gly Ala Gly Ser Ile Ser
145 150 155 160

Tyr Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln
165 170 175

Asn Asn Asn Arg Ala Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile
180 185 190

Val Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr
195 200 205

Ala Ser Leu Asn Gly Thr Ser Met Ala Thr Pro His Val Ala Gly Ala
210 215 220

Ala Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile
225 230 235 240

Arg Asn His Leu Lys Asn Thr Ala Thr Ser Leu Gly Ser Thr Asn Leu
245 250 255

Tyr Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Thr Arg
260 265

<210> 7
<211> 60
<212> DNA
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<220>
<223> synthetic oligopeptide

<220>

SEQ list 10203.ST25

<221> misc_feature
<222> (1)..(60)
<223> primer 28-35-CN

<400> 7
tagatctgga tgagtggawv yccctgtatc gaggacagcw rbttttacac cagaacctgt 60

<210> 8
<211> 18
<212> DNA
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<220>
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<220>
<221> misc_feature
<222> (1)..(18)
<223> primer 28-35-NC

<400> 8
tccactcatc cagatcta 18

<210> 9
<211> 45
<212> DNA
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<220>
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<220>
<221> misc_feature
<222> (1)..(45)
<223> primer 71-72-73-CN (I)

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<210> 10
<211> 45
<212> DNA
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<220>
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<220>
<221> misc_feature
<222> (1)..(45)
<223> primer 71-72-73-CN (II)

<400> 10
aatcgaattg tttaaagcaa gwvygwgccc ggccacatgc gtgcc 45

<210> 11
<211> 45
<212> DNA
<213> artificial

<220>

<223> synthetic oligopeptide

<220>

<221> misc_feature

<222> (1)..(45)

<223> primer 71-72-73-CN (III)

<400> 11

aatcgaattg tttaaagcgc cwvygwgccc ggccacatgc gtgcc

45

<210> 12

<211> 18

<212> DNA

<213> artificial

<220>

<223> synthetic oligopeptide

<220>

<221> misc_feature

<222> (1)..(18)

<223> primer 71-72-73-NC

<400> 12

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18

<210> 13

<211> 24

<212> DNA

<213> artificial

<220>

<223> synthetic oligopeptide

<220>

<221> misc_feature

<222> (1)..(24)

<223> primer 139

<400> 13

gattaacgcg ttgccgcttc tgcg

24

<210> 14

<211> 39

<212> DNA

<213> artificial

<220>

<223> synthetic oligopeptide

<220>

<221> misc_feature

<222> (1)..(39)

<223> primer 175-CN (I)

<400> 14

atcagtagct ccgactgccca ytgcgttcgc atagcgcgc

39

<210> 15

<211> 39

<212> DNA
<213> artificial

<220>
<223> synthetic oligopeptide

<220>
<221> misc_feature
<222> (1)..(39)
<223> primer 175-CN (II)

<400> 15
atcagtagct ccgactgccg ctgcgttcgc atagcgcgc

39

<210> 16
<211> 18
<212> DNA
<213> artificial

<220>
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<220>
<221> misc_feature
<222> (1)..(18)
<223> primer 175-NC

<400> 16
gcagtcggag ctactgat

18

<210> 17
<211> 39
<212> DNA
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<220>
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<220>
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<222> (1)..(39)
<223> primer 224-CN

<400> 17
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39

<210> 18
<211> 18
<212> DNA
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<220>
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<220>
<221> misc_feature
<222> (1)..(18)
<223> primer 224-NC

<400> 18
cctcatgttg caggtgcg

18

SEQ list 10203.ST25

<210> 19
<211> 22
<212> DNA
<213> artificial

<220>
<223> synthetic oligopeptide

<220>
<221> misc_feature
<222> (1)..(22)
<223> primer 317-CN

<400> 19
tggcgcaatc ggtaccatgg gg 22

<210> 20
<211> 936
<212> DNA
<213> TY145 subtilase DNA

<400> 20
gcggtaccaa gtacacaaac cccttggggc ataaagtcaa ttataaatga tcaatcaatt 60
acaaaaacaa ctggaggcag cggaattaag gtagctgttt tagatacagg ggtttataca 120
agccatttag atttagctgg ttctgccgag caatgcaagg attttaccga atctaatacct 180
ttagtagatg gttcatgcac cgatcgccaa gggcatggta cacatgttgc cggaactgta 240
ttggcgcatg gaggcagtaa tggacaaggc gtttacgggg tggctccgca agcgaaacta 300
tgggcatata aagtattagg agataacggc agcggatact ctgatgatat tgcagcagct 360
atcagacatg tagctgatga agcttcacgt acagggtcca aagtagtaat taatatgtcg 420
ctaggttcat ctgccaaagg ttcatgtatt gctagtgcag tagattatgc atatggaaaa 480
ggtgtattaa tcgttgctgc ggctggtaat agtgggtcag gcagcaatac aatcggcttt 540
cctggcgggc ttgtaaatgc agtggcagta gcggcattgg agaattgtca gcaaaatgga 600
acttatcgag tagctgattt ctcatctaga gggaatccgg caactgctgg agattatatt 660
attcaagagc gtgatattga agtttcagct ccgggagcaa gtgtagagtc tacatggtac 720
actggcgggt ataatacgat cagcgggtaca tcaatggcta cacctcatgt agctgggtta 780
gctgctaaaa tctggtcagc gaatacttca ttaagtcata gccaaactgcg cacagaattg 840
caaaatcgcg ctaaagtata tgatattaaa ggtgggtatcg gagccggaac aggtgacgat 900
tatgcatcag gggtcggata tccaagagta aaataa 936

<210> 21
<211> 1143
<212> DNA
<213> Bacillus lentus, Savinase

<400> 21
atgaagaaac cggtggggaa aattgtcgca agcaccgcac tactcatttc tgttgctttt 60
agttcatcga tcgcatcggc tgctgaagaa gcaaaagaaa aatatttaaat tggctttaat 120

SEQ list 10203.ST25

gagcaggaag ctgtcagtga gttttagtaa caagtagagg caaatgacga ggtcgccatt	180
ctctctgagg aagaggaagt cgaaattgaa ttgcttcatg aatttgaaac gattcctgtt	240
ttatccgttg agttaagccc agaagatgtg gacgcgcttg aactcgatcc agcgatttct	300
tatattgaag aggatgcaga agtaacgaca atggcgcaat cggtaccatg gggaattagc	360
cgtgtgcaag ccccagctgc ccataaccgt ggattgacag gttctggtgt aaaagttgct	420
gtcctcgata cagggatatc cactcatcca gatctaaata ttcgtggtgg cgcaagcttt	480
gtaccagggg aaccgtcgac tcaagatggg aatgggcatg gcacgcatgt ggccgggacg	540
atcgctgctt taaacaattc gattggcggt cttggcgtag cgccgagcgc tgagctatac	600
gctgttaaag tcctaggggc gagcggttca ggttcgggtca gctcgattgc ccaaggattg	660
gaatgggcag ggaacaatgg catgcacggt gctaatttga gtttaggaag cccttcgcca	720
agtgccacac tcgagcaagc tgtaaatagc gcgacttcta gaggcgttct tgttgtagcg	780
gcatctggga attcagggtc aggtcaatc agctatccgg cgcgctatgc gaacgcaatg	840
gcagtcggag ctactgatca aaacaacaac cgcgctagct tttcacagta tggcgcaggc	900
cttgacattg tcgcaccggt ggtaaacgtg cagagcacat acccagggtc aacatatgcc	960
agcttaaacg gtacatcgat ggctactcct catgttgtag gtgcggccgc ctttgtaaa	1020
caaaagaacc catcttggtc taatgtacaa attcgaaatc atctaaagaa tacggcaact	1080
agtttaggaa gcacgaactt gtatggaagc ggacttggtt acgcagaagc ggcaacgcgt	1140
taa	1143

NZ 10203.000-DK APPENDIX 1

REMARK 3 REFINEMENT.
 REMARK 3 PROGRAM : REFMAC 5.0
 REMARK 3 AUTHORS : MURSHUDOV,VAGIN,DODSON
 REMARK 3
 REMARK 3 REFINEMENT TARGET : MAXIMUM LIKELIHOOD
 REMARK 3
 REMARK 3 DATA USED IN REFINEMENT.
 REMARK 3 RESOLUTION RANGE HIGH (ANGSTROMS) : 1.80
 REMARK 3 RESOLUTION RANGE LOW (ANGSTROMS) : 56.80
 REMARK 3 DATA CUTOFF (SIGMA(F)) : NONE
 REMARK 3 COMPLETENESS FOR RANGE (%) : 99.88
 REMARK 3 NUMBER OF REFLECTIONS : 38045
 REMARK 3
 REMARK 3 FIT TO DATA USED IN REFINEMENT.
 REMARK 3 CROSS-VALIDATION METHOD : THROUGHOUT
 REMARK 3 FREE R VALUE TEST SET SELECTION : RANDOM
 REMARK 3 R VALUE (WORKING + TEST SET) : 0.15648
 REMARK 3 R VALUE (WORKING SET) : 0.15487
 REMARK 3 FREE R VALUE : 0.18707
 REMARK 3 FREE R VALUE TEST SET SIZE (%) : 5.0
 REMARK 3 FREE R VALUE TEST SET COUNT : 2009
 REMARK 3
 REMARK 3 FIT IN THE HIGHEST RESOLUTION BIN.
 REMARK 3 TOTAL NUMBER OF BINS USED : 20
 REMARK 3 BIN RESOLUTION RANGE HIGH : 1.796
 REMARK 3 BIN RESOLUTION RANGE LOW : 1.842
 REMARK 3 REFLECTION IN BIN (WORKING SET) : 2738
 REMARK 3 BIN R VALUE (WORKING SET) : 0.191
 REMARK 3 BIN FREE R VALUE SET COUNT : 138
 REMARK 3 BIN FREE R VALUE : 0.234
 REMARK 3
 REMARK 3 NUMBER OF NON-HYDROGEN ATOMS USED IN REFINEMENT.
 REMARK 3 ALL ATOMS : 3156
 REMARK 3
 REMARK 3 B VALUES.
 REMARK 3 FROM WILSON PLOT (A**2) : NULL
 REMARK 3 MEAN B VALUE (OVERALL, A**2) : 14.804
 REMARK 3 OVERALL ANISOTROPIC B VALUE.
 REMARK 3 B11 (A**2) : 0.28
 REMARK 3 B22 (A**2) : -0.86
 REMARK 3 B33 (A**2) : 0.58
 REMARK 3 B12 (A**2) : 0.00
 REMARK 3 B13 (A**2) : 0.00
 REMARK 3 B23 (A**2) : 0.00
 REMARK 3
 REMARK 3 ESTIMATED OVERALL COORDINATE ERROR.
 REMARK 3 ESU BASED ON R VALUE (A) : 0.100
 REMARK 3 ESU BASED ON FREE R VALUE (A) : 0.098
 REMARK 3 ESU BASED ON MAXIMUM LIKELIHOOD (A) : 0.093
 REMARK 3 ESU FOR B VALUES BASED ON MAXIMUM LIKELIHOOD (A**2) : 2.910
 REMARK 3
 REMARK 3 CORRELATION COEFFICIENTS.
 REMARK 3 CORRELATION COEFFICIENT FO-FC : 0.963
 REMARK 3 CORRELATION COEFFICIENT FO-FC FREE : 0.952
 REMARK 3

REMARK	3	RMS DEVIATIONS FROM IDEAL VALUES	COUNT	RMS	WEIGHT	
REMARK	3	BOND LENGTHS REFINED ATOMS (A):	2798	0.021	0.021	
REMARK	3	BOND LENGTHS OTHERS (A):	2500	0.001	0.020	
REMARK	3	BOND ANGLES REFINED ATOMS (DEGREES):	3805	1.859	1.943	
REMARK	3	BOND ANGLES OTHERS (DEGREES):	5821	0.854	3.000	
REMARK	3	TORSION ANGLES, PERIOD 1 (DEGREES):	372	5.125	3.000	
REMARK	3	TORSION ANGLES, PERIOD 3 (DEGREES):	462	16.877	15.000	
REMARK	3	CHIRAL-CENTER RESTRAINTS (A**3):	437	0.119	0.200	
REMARK	3	GENERAL PLANES REFINED ATOMS (A):	3201	0.009	0.020	
REMARK	3	GENERAL PLANES OTHERS (A):	535	0.004	0.020	
REMARK	3	NON-BONDED CONTACTS REFINED ATOMS (A):	610	0.228	0.300	
REMARK	3	NON-BONDED CONTACTS OTHERS (A):	2548	0.203	0.300	
REMARK	3	H-BOND (X...Y) REFINED ATOMS (A):	374	0.184	0.500	
REMARK	3	H-BOND (X...Y) OTHERS (A):	3	0.279	0.500	
REMARK	3	POTENTIAL METAL-ION REFINED ATOMS (A):	16	0.119	0.500	
REMARK	3	SYMMETRY VDW REFINED ATOMS (A):	7	0.127	0.300	
REMARK	3	SYMMETRY VDW OTHERS (A):	27	0.152	0.300	
REMARK	3	SYMMETRY H-BOND REFINED ATOMS (A):	37	0.278	0.500	
REMARK	3	ISOTROPIC THERMAL FACTOR RESTRAINTS.	COUNT	RMS	WEIGHT	
REMARK	3	MAIN-CHAIN BOND REFINED ATOMS (A**2):	1840	1.131	1.500	
REMARK	3	MAIN-CHAIN ANGLE REFINED ATOMS (A**2):	2941	1.781	2.000	
REMARK	3	SIDE-CHAIN BOND REFINED ATOMS (A**2):	958	2.873	3.000	
REMARK	3	SIDE-CHAIN ANGLE REFINED ATOMS (A**2):	864	4.300	4.500	
REMARK	3	NCS RESTRAINTS STATISTICS				
REMARK	3	NUMBER OF NCS GROUPS : NULL				
REMARK	3	TLs DETAILS				
REMARK	3	NUMBER OF TLs GROUPS : NULL				
REMARK	3	BULK SOLVENT MODELLING.				
REMARK	3	METHOD USED : BABINET MODEL WITH MASK				
REMARK	3	PARAMETERS FOR MASK CALCULATION				
REMARK	3	VDW PROBE RADIUS : 1.40				
REMARK	3	ION PROBE RADIUS : 0.80				
REMARK	3	SHRINKAGE RADIUS : 0.80				
REMARK	3	OTHER REFINEMENT REMARKS:				
REMARK	3	HYDROGENS HAVE BEEN ADDED IN THE RIDING POSITIONS				
CISPEP	1	GLY A 172 SER A 173	0.00			
CISPEP	2	PHE A 180 PRO A 181	0.00			
SSBOND	1	CYS A 52 CYS A 66				
CRYST1	58.753	66.838 107.082 90.00 90.00 90.00 P 21 21 21				
SCALE1	0.017020	0.000000 0.000000 0.000000	0.000000			
SCALE2	0.000000	0.014962 0.000000 0.000000	0.000000			
SCALE3	0.000000	0.000000 0.009339 0.000000	0.000000			
ATOM	1	N ALA A 1	2.336	20.870	1.027 1.00 27.48	N
ATOM	3	CA ALA A 1	1.951	20.940	2.465 1.00 29.42	C
ATOM	5	CB ALA A 1	2.391	19.637	3.197 1.00 29.45	C
ATOM	9	C ALA A 1	2.665	22.149	3.096 1.00 28.87	C
ATOM	10	O ALA A 1	3.696	22.577	2.627 1.00 30.49	O
ATOM	13	N VAL A 2	2.014	22.747	4.052 1.00 30.31	N
ATOM	15	CA VAL A 2	2.658	23.754	4.877 1.00 30.69	C
ATOM	17	CB VAL A 2	2.068	25.139	4.604 1.00 30.94	C

ATOM	19	CG1	VAL	A	2	2.611	25.702	3.252	1.00	32.62	C
ATOM	23	CG2	VAL	A	2	0.577	25.086	4.667	1.00	30.84	C
ATOM	27	C	VAL	A	2	2.494	23.346	6.347	1.00	29.48	C
ATOM	28	O	VAL	A	2	1.580	22.610	6.743	1.00	29.33	O
ATOM	29	N	PRO	A	3	3.412	23.788	7.186	1.00	28.10	N
ATOM	30	CA	PRO	A	3	3.298	23.380	8.581	1.00	27.90	C
ATOM	32	CB	PRO	A	3	4.645	23.830	9.185	1.00	26.48	C
ATOM	35	CG	PRO	A	3	5.116	24.998	8.340	1.00	26.57	C
ATOM	38	CD	PRO	A	3	4.530	24.697	6.933	1.00	27.60	C
ATOM	41	C	PRO	A	3	2.129	24.112	9.216	1.00	27.01	C
ATOM	42	O	PRO	A	3	1.602	25.037	8.600	1.00	28.48	O
ATOM	43	N	SER	A	4	1.767	23.774	10.434	1.00	26.37	N
ATOM	45	CA	SER	A	4	0.718	24.505	11.159	1.00	25.29	C
ATOM	47	CB	SER	A	4	0.279	23.780	12.444	1.00	26.52	C
ATOM	50	OG	SER	A	4	1.173	23.913	13.554	1.00	25.41	O
ATOM	52	C	SER	A	4	1.105	25.956	11.445	1.00	26.09	C
ATOM	53	O	SER	A	4	0.212	26.810	11.603	1.00	25.32	O
ATOM	54	N	THR	A	5	2.415	26.233	11.497	1.00	24.12	N
ATOM	56	CA	THR	A	5	3.023	27.567	11.741	1.00	22.81	C
ATOM	58	CB	THR	A	5	3.009	28.007	13.237	1.00	24.21	C
ATOM	60	OG1	THR	A	5	3.793	29.191	13.386	1.00	23.29	O
ATOM	62	CG2	THR	A	5	3.727	26.999	14.151	1.00	22.71	C
ATOM	66	C	THR	A	5	4.413	27.436	11.219	1.00	23.10	C
ATOM	67	O	THR	A	5	5.012	26.322	11.267	1.00	21.48	O
ATOM	68	N	GLN	A	6	4.959	28.518	10.692	1.00	21.30	N
ATOM	70	CA	GLN	A	6	6.260	28.438	10.102	1.00	21.50	C
ATOM	72	CB	GLN	A	6	6.512	29.634	9.209	1.00	22.77	C
ATOM	75	CG	GLN	A	6	5.626	29.570	7.926	1.00	23.15	C
ATOM	78	CD	GLN	A	6	5.999	30.579	6.911	1.00	28.40	C
ATOM	79	OE1	GLN	A	6	5.356	31.619	6.822	1.00	30.34	O
ATOM	80	NE2	GLN	A	6	7.016	30.300	6.133	1.00	24.59	N
ATOM	83	C	GLN	A	6	7.295	28.389	11.185	1.00	20.24	C
ATOM	84	O	GLN	A	6	8.438	28.017	10.927	1.00	18.46	O
ATOM	85	N	THR	A	7	6.870	28.777	12.378	1.00	18.84	N
ATOM	87	CA	THR	A	7	7.752	28.808	13.565	1.00	19.27	C
ATOM	89	CB	THR	A	7	8.135	30.238	13.914	1.00	19.55	C
ATOM	91	OG1	THR	A	7	6.958	31.041	14.091	1.00	23.00	O
ATOM	93	CG2	THR	A	7	8.910	30.878	12.842	1.00	19.61	C
ATOM	97	C	THR	A	7	7.111	28.128	14.755	1.00	18.28	C
ATOM	98	O	THR	A	7	6.436	28.735	15.547	1.00	18.57	O
ATOM	99	N	PRO	A	8	7.288	26.803	14.834	1.00	17.34	N
ATOM	100	CA	PRO	A	8	6.795	26.000	15.922	1.00	17.79	C
ATOM	102	CB	PRO	A	8	7.459	24.615	15.659	1.00	17.18	C
ATOM	105	CG	PRO	A	8	7.556	24.570	14.138	1.00	18.32	C
ATOM	108	CD	PRO	A	8	7.961	25.984	13.814	1.00	16.59	C
ATOM	111	C	PRO	A	8	7.162	26.584	17.273	1.00	16.99	C
ATOM	112	O	PRO	A	8	8.105	27.339	17.369	1.00	18.02	O
ATOM	113	N	TRP	A	9	6.426	26.203	18.280	1.00	18.21	N
ATOM	115	CA	TRP	A	9	6.613	26.750	19.611	1.00	17.56	C
ATOM	117	CB	TRP	A	9	5.723	26.059	20.603	1.00	17.84	C
ATOM	120	CG	TRP	A	9	6.129	24.806	21.197	1.00	14.36	C
ATOM	121	CD1	TRP	A	9	5.772	23.569	20.796	1.00	15.37	C
ATOM	123	NE1	TRP	A	9	6.278	22.630	21.658	1.00	15.66	N
ATOM	125	CE2	TRP	A	9	7.033	23.276	22.609	1.00	16.83	C
ATOM	126	CD2	TRP	A	9	6.952	24.642	22.345	1.00	14.81	C
ATOM	127	CE3	TRP	A	9	7.642	25.531	23.186	1.00	14.62	C
ATOM	129	CZ3	TRP	A	9	8.362	24.982	24.301	1.00	11.92	C
ATOM	131	CH2	TRP	A	9	8.393	23.626	24.526	1.00	15.97	C

ATOM	133	CZ2	TRP	A	9	7.757	22.750	23.677	1.00	14.67	C
ATOM	135	C	TRP	A	9	8.073	26.760	20.083	1.00	18.17	C
ATOM	136	O	TRP	A	9	8.531	27.737	20.662	1.00	15.91	O
ATOM	137	N	GLY	A	10	8.780	25.675	19.859	1.00	16.36	N
ATOM	139	CA	GLY	A	10	10.180	25.618	20.307	1.00	15.48	C
ATOM	142	C	GLY	A	10	11.108	26.619	19.663	1.00	15.80	C
ATOM	143	O	GLY	A	10	12.089	27.060	20.254	1.00	14.71	O
ATOM	144	N	ILE	A	11	10.801	26.939	18.410	1.00	15.18	N
ATOM	146	CA	ILE	A	11	11.599	27.866	17.642	1.00	15.64	C
ATOM	148	CB	ILE	A	11	11.303	27.768	16.151	1.00	14.65	C
ATOM	150	CG1	ILE	A	11	11.479	26.328	15.653	1.00	15.91	C
ATOM	153	CD1	ILE	A	11	12.945	25.811	15.725	1.00	16.96	C
ATOM	157	CG2	ILE	A	11	12.204	28.704	15.385	1.00	16.09	C
ATOM	161	C	ILE	A	11	11.291	29.225	18.193	1.00	15.73	C
ATOM	162	O	ILE	A	11	12.197	29.995	18.438	1.00	15.02	O
ATOM	163	N	LYS	A	12	10.005	29.552	18.352	1.00	16.62	N
ATOM	165	CA	LYS	A	12	9.649	30.832	18.949	1.00	16.28	C
ATOM	167	CB	LYS	A	12	8.147	30.926	19.078	1.00	17.21	C
ATOM	170	CG	LYS	A	12	7.419	31.148	17.707	1.00	20.12	C
ATOM	173	CD	LYS	A	12	5.874	31.303	17.997	1.00	20.50	C
ATOM	176	CE	LYS	A	12	5.137	31.855	16.795	1.00	28.93	C
ATOM	179	NZ	LYS	A	12	4.564	30.819	15.858	1.00	19.42	N
ATOM	183	C	LYS	A	12	10.242	30.956	20.345	1.00	15.82	C
ATOM	184	O	LYS	A	12	10.790	32.014	20.745	1.00	15.87	O
ATOM	185	N	SER	A	13	10.172	29.865	21.075	1.00	13.09	N
ATOM	187	CA	SER	A	13	10.655	29.893	22.450	1.00	13.64	C
ATOM	189	CB	SER	A	13	10.284	28.586	23.149	1.00	12.46	C
ATOM	192	OG	SER	A	13	10.790	28.548	24.491	1.00	14.12	O
ATOM	194	C	SER	A	13	12.167	30.131	22.519	1.00	12.81	C
ATOM	195	O	SER	A	13	12.650	30.959	23.323	1.00	11.51	O
ATOM	196	N	ILE	A	14	12.931	29.371	21.752	1.00	12.90	N
ATOM	198	CA	ILE	A	14	14.391	29.521	21.839	1.00	13.05	C
ATOM	200	CB	ILE	A	14	15.108	28.318	21.206	1.00	12.73	C
ATOM	202	CG1	ILE	A	14	16.498	28.183	21.810	1.00	13.73	C
ATOM	205	CD1	ILE	A	14	17.265	26.959	21.415	1.00	17.32	C
ATOM	209	CG2	ILE	A	14	15.161	28.394	19.753	1.00	14.13	C
ATOM	213	C	ILE	A	14	14.869	30.861	21.299	1.00	14.41	C
ATOM	214	O	ILE	A	14	15.907	31.367	21.680	1.00	15.23	O
ATOM	215	N	TYR	A	15	14.094	31.423	20.389	1.00	15.25	N
ATOM	217	CA	TYR	A	15	14.392	32.753	19.877	1.00	16.87	C
ATOM	219	CB	TYR	A	15	13.742	32.965	18.490	1.00	15.13	C
ATOM	222	CG	TYR	A	15	14.683	32.629	17.348	1.00	16.40	C
ATOM	223	CD1	TYR	A	15	14.956	31.303	17.008	1.00	14.01	C
ATOM	225	CE1	TYR	A	15	15.834	30.998	16.024	1.00	16.36	C
ATOM	227	CZ	TYR	A	15	16.453	31.993	15.321	1.00	16.82	C
ATOM	228	OH	TYR	A	15	17.364	31.738	14.329	1.00	15.20	O
ATOM	230	CE2	TYR	A	15	16.182	33.303	15.621	1.00	17.27	C
ATOM	232	CD2	TYR	A	15	15.320	33.610	16.628	1.00	16.64	C
ATOM	234	C	TYR	A	15	13.925	33.826	20.856	1.00	16.27	C
ATOM	235	O	TYR	A	15	14.311	35.008	20.744	1.00	17.84	O
ATOM	236	N	ASN	A	16	13.075	33.432	21.780	1.00	17.21	N
ATOM	238	CA	ASN	A	16	12.534	34.334	22.811	1.00	17.53	C
ATOM	240	CB	ASN	A	16	13.628	34.860	23.743	1.00	16.83	C
ATOM	243	CG	ASN	A	16	13.098	35.265	25.103	1.00	18.27	C
ATOM	244	OD1	ASN	A	16	11.901	35.461	25.288	1.00	21.90	O
ATOM	245	ND2	ASN	A	16	13.987	35.324	26.075	1.00	17.31	N
ATOM	248	C	ASN	A	16	11.788	35.480	22.114	1.00	19.04	C
ATOM	249	O	ASN	A	16	11.940	36.642	22.463	1.00	18.19	O

ATOM	250	N	ASP	A	17	10.972	35.107	21.135	1.00	18.56	N
ATOM	252	CA	ASP	A	17	10.176	36.069	20.372	1.00	19.69	C
ATOM	254	CB	ASP	A	17	11.019	36.634	19.287	1.00	19.45	C
ATOM	257	CG	ASP	A	17	10.362	37.812	18.579	1.00	20.65	C
ATOM	258	OD1	ASP	A	17	9.160	38.017	18.745	1.00	24.61	O
ATOM	259	OD2	ASP	A	17	11.034	38.547	17.849	1.00	19.73	O
ATOM	260	C	ASP	A	17	8.937	35.412	19.778	1.00	19.80	C
ATOM	261	O	ASP	A	17	9.032	34.693	18.834	1.00	22.05	O
ATOM	262	N	GLN	A	18	7.791	35.647	20.369	1.00	20.51	N
ATOM	264	CA	GLN	A	18	6.593	34.957	19.960	1.00	21.49	C
ATOM	266	CB	GLN	A	18	5.549	35.062	21.054	1.00	22.51	C
ATOM	269	CG	GLN	A	18	5.917	34.348	22.318	1.00	24.55	C
ATOM	272	CD	GLN	A	18	6.243	32.907	22.041	1.00	29.84	C
ATOM	273	OE1	GLN	A	18	7.347	32.450	22.314	1.00	31.44	O
ATOM	274	NE2	GLN	A	18	5.301	32.204	21.457	1.00	28.00	N
ATOM	277	C	GLN	A	18	6.076	35.511	18.658	1.00	21.92	C
ATOM	278	O	GLN	A	18	5.213	34.911	18.021	1.00	22.98	O
ATOM	279	N	SER	A	19	6.697	36.572	18.185	1.00	22.89	N
ATOM	281	CA	SER	A	19	6.231	37.202	16.951	1.00	23.92	C
ATOM	283	CB	SER	A	19	6.338	38.715	17.096	1.00	23.69	C
ATOM	286	OG	SER	A	19	7.627	39.225	16.746	1.00	25.66	O
ATOM	288	C	SER	A	19	6.947	36.728	15.670	1.00	24.30	C
ATOM	289	O	SER	A	19	6.454	36.972	14.566	1.00	25.69	O
ATOM	290	N	ILE	A	20	8.079	36.029	15.764	1.00	23.62	N
ATOM	292	CA	ILE	A	20	8.791	35.673	14.529	1.00	23.92	C
ATOM	294	CB	ILE	A	20	10.104	34.965	14.836	1.00	24.53	C
ATOM	296	CG1	ILE	A	20	9.858	33.755	15.727	1.00	22.48	C
ATOM	299	CD1	ILE	A	20	11.041	32.826	15.641	1.00	23.83	C
ATOM	303	CG2	ILE	A	20	11.127	35.902	15.477	1.00	27.13	C
ATOM	307	C	ILE	A	20	8.011	34.784	13.573	1.00	23.40	C
ATOM	308	O	ILE	A	20	7.241	33.913	13.999	1.00	24.30	O
ATOM	309	N	THR	A	21	8.295	34.963	12.296	1.00	23.97	N
ATOM	311	CA	THR	A	21	7.686	34.184	11.215	1.00	24.95	C
ATOM	313	CB	THR	A	21	6.856	35.107	10.283	1.00	24.97	C
ATOM	315	OG1	THR	A	21	7.690	36.186	9.842	1.00	27.61	O
ATOM	317	CG2	THR	A	21	5.771	35.794	11.039	1.00	28.02	C
ATOM	321	C	THR	A	21	8.799	33.570	10.392	1.00	23.92	C
ATOM	322	O	THR	A	21	8.544	32.865	9.419	1.00	23.90	O
ATOM	323	N	LYS	A	22	10.044	33.862	10.735	1.00	23.93	N
ATOM	325	CA	LYS	A	22	11.148	33.239	10.041	1.00	24.18	C
ATOM	327	CB	LYS	A	22	11.386	33.880	8.675	1.00	25.22	C
ATOM	330	CG	LYS	A	22	11.830	35.314	8.724	1.00	28.95	C
ATOM	333	CD	LYS	A	22	12.397	35.808	7.348	1.00	32.55	C
ATOM	336	CE	LYS	A	22	13.701	35.129	6.988	0.10	31.56	C
ATOM	339	NZ	LYS	A	22	14.274	35.671	5.722	0.10	31.66	N
ATOM	343	C	LYS	A	22	12.406	33.333	10.903	1.00	23.63	C
ATOM	344	O	LYS	A	22	12.471	34.145	11.823	1.00	24.17	O
ATOM	345	N	THR	A	23	13.395	32.491	10.628	1.00	21.41	N
ATOM	347	CA	THR	A	23	14.661	32.526	11.342	1.00	20.21	C
ATOM	349	CB	THR	A	23	14.914	31.202	12.030	1.00	20.28	C
ATOM	351	OG1	THR	A	23	14.859	30.158	11.034	1.00	19.28	O
ATOM	353	CG2	THR	A	23	13.846	30.915	13.074	1.00	21.44	C
ATOM	357	C	THR	A	23	15.785	32.791	10.384	1.00	20.28	C
ATOM	358	O	THR	A	23	15.565	32.740	9.182	1.00	19.80	O
ATOM	359	N	THR	A	24	16.996	33.027	10.908	1.00	19.65	N
ATOM	361	CA	THR	A	24	18.201	33.246	10.130	1.00	19.91	C
ATOM	363	CB	THR	A	24	18.532	34.784	9.840	1.00	21.93	C
ATOM	365	OG1	THR	A	24	18.685	35.435	11.102	1.00	25.69	O

ATOM	367	CG2	THR	A	24	17.402	35.514	9.229	1.00	25.02	C
ATOM	371	C	THR	A	24	19.407	32.743	10.928	1.00	19.55	O
ATOM	372	O	THR	A	24	19.372	32.551	12.149	1.00	19.70	C
ATOM	373	N	GLY	A	25	20.473	32.497	10.225	1.00	17.41	N
ATOM	375	CA	GLY	A	25	21.716	32.187	10.893	1.00	17.64	C
ATOM	378	C	GLY	A	25	22.286	30.799	10.641	1.00	16.16	C
ATOM	379	O	GLY	A	25	21.583	29.936	10.124	1.00	15.92	O
ATOM	380	N	GLY	A	26	23.548	30.620	11.068	1.00	15.49	N
ATOM	382	CA	GLY	A	26	24.296	29.380	10.938	1.00	15.44	C
ATOM	385	C	GLY	A	26	25.166	29.220	9.692	1.00	15.61	C
ATOM	386	O	GLY	A	26	25.782	28.199	9.493	1.00	15.36	O
ATOM	387	N	SER	A	27	25.264	30.249	8.861	1.00	17.72	N
ATOM	389	CA	SER	A	27	26.108	30.182	7.691	1.00	18.45	C
ATOM	391	CB	SER	A	27	25.990	31.500	6.837	1.00	20.08	C
ATOM	394	OG	SER	A	27	26.686	32.496	7.490	1.00	26.34	O
ATOM	396	C	SER	A	27	27.534	29.838	8.029	1.00	17.45	C
ATOM	397	O	SER	A	27	28.166	30.341	8.969	1.00	17.59	O
ATOM	398	N	GLY	A	28	28.071	28.913	7.241	1.00	16.01	N
ATOM	400	CA	GLY	A	28	29.421	28.494	7.385	1.00	16.46	C
ATOM	403	C	GLY	A	28	29.615	27.360	8.377	1.00	15.36	C
ATOM	404	O	GLY	A	28	30.739	26.917	8.527	1.00	16.82	O
ATOM	405	N	ILE	A	29	28.587	26.931	9.076	1.00	14.25	N
ATOM	407	CA	ILE	A	29	28.782	25.832	10.044	1.00	13.92	C
ATOM	409	CB	ILE	A	29	28.057	26.170	11.335	1.00	14.10	C
ATOM	411	CG1	ILE	A	29	28.482	27.563	11.856	1.00	13.61	C
ATOM	414	CD1	ILE	A	29	29.986	27.710	12.081	1.00	15.86	C
ATOM	418	CG2	ILE	A	29	28.269	25.076	12.417	1.00	14.40	C
ATOM	422	C	ILE	A	29	28.143	24.586	9.459	1.00	14.30	C
ATOM	423	O	ILE	A	29	27.190	24.708	8.690	1.00	14.55	O
ATOM	424	N	LYS	A	30	28.614	23.402	9.853	1.00	13.73	N
ATOM	426	CA	LYS	A	30	28.008	22.173	9.422	1.00	13.73	C
ATOM	428	CB	LYS	A	30	29.019	21.204	8.860	1.00	14.64	C
ATOM	431	CG	LYS	A	30	30.072	21.822	7.951	1.00	15.03	C
ATOM	434	CD	LYS	A	30	29.438	22.566	6.745	1.00	16.42	C
ATOM	437	CE	LYS	A	30	30.497	23.364	5.987	1.00	19.44	C
ATOM	440	NZ	LYS	A	30	29.865	24.009	4.752	1.00	17.01	N
ATOM	444	C	LYS	A	30	27.354	21.482	10.655	1.00	13.57	C
ATOM	445	O	LYS	A	30	27.978	21.473	11.716	1.00	14.48	O
ATOM	446	N	VAL	A	31	26.163	20.941	10.498	1.00	13.11	N
ATOM	448	CA	VAL	A	31	25.572	20.118	11.583	1.00	13.65	C
ATOM	450	CB	VAL	A	31	24.249	20.639	12.061	1.00	13.16	C
ATOM	452	CG1	VAL	A	31	23.726	19.743	13.173	1.00	15.78	C
ATOM	456	CG2	VAL	A	31	24.401	22.058	12.573	1.00	12.55	C
ATOM	460	C	VAL	A	31	25.470	18.708	11.047	1.00	14.30	C
ATOM	461	O	VAL	A	31	24.828	18.458	10.003	1.00	14.74	O
ATOM	462	N	ALA	A	32	26.129	17.789	11.737	1.00	14.62	N
ATOM	464	CA	ALA	A	32	26.092	16.387	11.366	1.00	13.46	C
ATOM	466	CB	ALA	A	32	27.419	15.728	11.606	1.00	11.29	C
ATOM	470	C	ALA	A	32	24.972	15.696	12.149	1.00	13.08	C
ATOM	471	O	ALA	A	32	25.056	15.556	13.393	1.00	12.55	O
ATOM	472	N	VAL	A	33	23.916	15.340	11.435	1.00	10.76	N
ATOM	474	CA	VAL	A	33	22.778	14.654	12.038	1.00	11.75	C
ATOM	476	CB	VAL	A	33	21.468	15.152	11.453	1.00	11.00	C
ATOM	478	CG1	VAL	A	33	20.317	14.313	11.935	1.00	13.80	C
ATOM	482	CG2	VAL	A	33	21.268	16.618	11.738	1.00	12.19	C
ATOM	486	C	VAL	A	33	22.959	13.155	11.847	1.00	12.72	C
ATOM	487	O	VAL	A	33	22.830	12.623	10.715	1.00	11.99	O
ATOM	488	N	LEU	A	34	23.290	12.466	12.932	1.00	12.34	N

ATOM	490	CA	LEU	A	34	23.599	11.022	12.949	1.00	11.72	C
ATOM	492	CB	LEU	A	34	24.811	10.744	13.878	1.00	11.57	C
ATOM	495	CG	LEU	A	34	26.190	10.819	13.262	1.00	11.59	C
ATOM	497	CD1	LEU	A	34	26.515	12.228	12.621	1.00	10.38	C
ATOM	501	CD2	LEU	A	34	27.275	10.414	14.265	1.00	12.17	C
ATOM	505	C	LEU	A	34	22.303	10.366	13.416	1.00	12.33	C
ATOM	506	O	LEU	A	34	21.964	10.409	14.581	1.00	11.53	O
ATOM	507	N	ASP	A	35	21.571	9.765	12.490	1.00	11.34	N
ATOM	509	CA	ASP	A	35	20.224	9.416	12.794	1.00	11.07	C
ATOM	511	CB	ASP	A	35	19.397	10.677	12.779	1.00	12.91	C
ATOM	514	CG	ASP	A	35	18.231	10.611	13.697	1.00	11.93	C
ATOM	515	OD1	ASP	A	35	17.334	9.791	13.472	1.00	12.81	O
ATOM	516	OD2	ASP	A	35	18.166	11.390	14.700	1.00	15.59	O
ATOM	517	C	ASP	A	35	19.687	8.393	11.816	1.00	12.34	C
ATOM	518	O	ASP	A	35	20.470	7.623	11.250	1.00	12.33	O
ATOM	519	N	THR	A	36	18.376	8.385	11.604	1.00	12.33	N
ATOM	521	CA	THR	A	36	17.783	7.395	10.702	1.00	13.86	C
ATOM	523	CB	THR	A	36	16.312	7.198	10.972	1.00	13.36	C
ATOM	525	OG1	THR	A	36	15.603	8.446	10.753	1.00	14.42	C
ATOM	527	CG2	THR	A	36	16.058	6.781	12.383	1.00	11.98	C
ATOM	531	C	THR	A	36	17.933	7.710	9.199	1.00	14.93	C
ATOM	532	O	THR	A	36	17.341	7.023	8.379	1.00	15.02	O
ATOM	533	N	GLY	A	37	18.699	8.735	8.885	1.00	15.27	N
ATOM	535	CA	GLY	A	37	18.838	9.282	7.530	1.00	15.54	C
ATOM	538	C	GLY	A	37	18.041	10.594	7.487	1.00	16.06	C
ATOM	539	O	GLY	A	37	17.413	10.973	8.482	1.00	14.08	O
ATOM	540	N	VAL	A	38	18.065	11.292	6.337	1.00	16.27	N
ATOM	542	CA	VAL	A	38	17.315	12.547	6.177	1.00	15.20	C
ATOM	544	CB	VAL	A	38	18.214	13.784	6.447	1.00	15.83	C
ATOM	546	CG1	VAL	A	38	17.501	15.075	6.182	1.00	16.87	C
ATOM	550	CG2	VAL	A	38	18.774	13.766	7.839	1.00	17.47	C
ATOM	554	C	VAL	A	38	16.863	12.628	4.695	1.00	16.04	C
ATOM	555	O	VAL	A	38	17.622	12.277	3.793	1.00	14.66	O
ATOM	556	N	TYR	A	39	15.623	13.008	4.532	1.00	18.21	N
ATOM	558	CA	TYR	A	39	15.046	13.247	3.214	1.00	19.90	C
ATOM	560	CB	TYR	A	39	13.564	13.150	3.366	1.00	18.60	C
ATOM	563	CG	TYR	A	39	12.795	13.480	2.082	1.00	23.59	C
ATOM	564	CD1	TYR	A	39	13.278	13.110	0.833	1.00	27.19	C
ATOM	566	CE1	TYR	A	39	12.555	13.413	-0.309	1.00	30.38	C
ATOM	568	CZ	TYR	A	39	11.391	14.129	-0.226	1.00	31.18	C
ATOM	569	OH	TYR	A	39	10.734	14.412	-1.434	1.00	30.34	O
ATOM	571	CE2	TYR	A	39	10.912	14.528	1.005	1.00	29.74	C
ATOM	573	CD2	TYR	A	39	11.623	14.208	2.144	1.00	23.70	C
ATOM	575	C	TYR	A	39	15.495	14.623	2.786	1.00	19.47	C
ATOM	576	O	TYR	A	39	14.795	15.631	2.992	1.00	22.39	O
ATOM	577	N	THR	A	40	16.675	14.659	2.240	1.00	22.23	N
ATOM	579	CA	THR	A	40	17.366	15.869	1.904	1.00	23.84	C
ATOM	581	CB	THR	A	40	18.797	15.520	1.499	1.00	25.17	C
ATOM	583	OG1	THR	A	40	18.841	14.473	0.518	1.00	27.20	O
ATOM	585	CG2	THR	A	40	19.633	14.890	2.687	1.00	23.66	C
ATOM	589	C	THR	A	40	16.650	16.659	0.804	1.00	25.31	C
ATOM	590	O	THR	A	40	17.008	17.803	0.566	1.00	25.93	O
ATOM	591	N	SER	A	41	15.671	16.051	0.147	1.00	25.63	N
ATOM	593	CA	SER	A	41	14.953	16.703	-0.942	1.00	26.05	C
ATOM	595	CB	SER	A	41	14.662	15.676	-2.047	1.00	25.60	C
ATOM	598	OG	SER	A	41	15.836	15.411	-2.759	1.00	26.14	O
ATOM	600	C	SER	A	41	13.669	17.317	-0.445	1.00	26.09	C
ATOM	601	O	SER	A	41	12.896	17.889	-1.232	1.00	26.66	O

ATOM	602	N	HIS	A	42	13.366	17.179	0.857	1.00	22.90	N
ATOM	604	CA	HIS	A	42	12.245	17.917	1.419	1.00	21.28	C
ATOM	606	CB	HIS	A	42	12.224	17.792	2.927	1.00	21.28	C
ATOM	609	CG	HIS	A	42	10.988	18.267	3.562	1.00	18.79	C
ATOM	610	ND1	HIS	A	42	10.616	19.591	3.556	1.00	17.72	N
ATOM	612	CE1	HIS	A	42	9.482	19.706	4.197	1.00	14.42	C
ATOM	614	NE2	HIS	A	42	9.124	18.516	4.654	1.00	18.07	N
ATOM	616	CD2	HIS	A	42	10.028	17.601	4.230	1.00	15.85	C
ATOM	618	C	HIS	A	42	12.427	19.379	1.036	1.00	20.43	C
ATOM	619	O	HIS	A	42	13.543	19.890	1.077	1.00	19.85	O
ATOM	620	N	LEU	A	43	11.326	20.044	0.686	1.00	21.20	N
ATOM	622	CA	LEU	A	43	11.380	21.409	0.210	1.00	21.25	C
ATOM	624	CB	LEU	A	43	10.030	21.945	-0.087	1.00	22.55	C
ATOM	627	CG	LEU	A	43	9.448	21.512	-1.433	1.00	25.81	C
ATOM	629	CD1	LEU	A	43	8.021	21.976	-1.464	1.00	27.58	C
ATOM	633	CD2	LEU	A	43	10.234	22.108	-2.559	1.00	27.86	C
ATOM	637	C	LEU	A	43	12.023	22.311	1.227	1.00	21.05	C
ATOM	638	O	LEU	A	43	12.699	23.255	0.879	1.00	18.87	O
ATOM	639	N	ASP	A	44	11.847	22.042	2.500	1.00	21.71	N
ATOM	641	CA	ASP	A	44	12.514	22.885	3.487	1.00	20.87	C
ATOM	643	CB	ASP	A	44	11.642	22.917	4.719	1.00	21.17	C
ATOM	646	CG	ASP	A	44	10.262	23.417	4.441	1.00	23.00	C
ATOM	647	OD1	ASP	A	44	10.060	24.154	3.406	1.00	21.93	O
ATOM	648	OD2	ASP	A	44	9.325	23.156	5.206	1.00	16.28	O
ATOM	649	C	ASP	A	44	13.962	22.528	3.812	1.00	21.02	C
ATOM	650	O	ASP	A	44	14.593	23.214	4.604	1.00	18.05	O
ATOM	651	N	LEU	A	45	14.488	21.431	3.252	1.00	18.30	N
ATOM	653	CA	LEU	A	45	15.868	21.070	3.445	1.00	19.90	C
ATOM	655	CB	LEU	A	45	15.922	19.624	4.024	1.00	18.80	C
ATOM	658	CG	LEU	A	45	15.174	19.394	5.300	1.00	18.65	C
ATOM	660	CD1	LEU	A	45	15.424	17.925	5.756	1.00	18.05	C
ATOM	664	CD2	LEU	A	45	15.714	20.351	6.357	1.00	20.33	C
ATOM	668	C	LEU	A	45	16.750	21.110	2.197	1.00	20.37	C
ATOM	669	O	LEU	A	45	17.960	20.890	2.251	1.00	22.13	O
ATOM	670	N	ALA	A	46	16.104	21.400	1.079	1.00	22.51	N
ATOM	672	CA	ALA	A	46	16.728	21.327	-0.210	1.00	21.13	C
ATOM	674	CB	ALA	A	46	15.738	21.695	-1.365	1.00	21.15	C
ATOM	678	C	ALA	A	46	17.880	22.199	-0.244	1.00	20.28	C
ATOM	679	O	ALA	A	46	17.806	23.344	0.177	1.00	22.66	O
ATOM	680	N	GLY	A	47	18.959	21.639	-0.759	1.00	20.67	N
ATOM	682	CA	GLY	A	47	20.217	22.320	-0.968	1.00	21.84	C
ATOM	685	C	GLY	A	47	21.042	22.419	0.291	1.00	21.53	C
ATOM	686	O	GLY	A	47	22.226	22.881	0.280	1.00	24.34	O
ATOM	687	N	SER	A	48	20.522	21.910	1.392	1.00	22.52	N
ATOM	689	CA	SER	A	48	21.310	21.980	2.610	1.00	21.98	C
ATOM	691	CB	ASER	A	48	20.384	22.083	3.833	0.50	22.54	C
ATOM	692	CB	BSER	A	48	20.408	22.073	3.814	0.50	22.26	C
ATOM	697	OG	ASER	A	48	19.449	21.001	3.944	0.50	23.88	O
ATOM	698	OG	BSER	A	48	19.660	23.258	3.738	0.50	21.10	O
ATOM	701	C	SER	A	48	22.295	20.852	2.826	1.00	21.47	C
ATOM	702	O	SER	A	48	23.317	21.066	3.466	1.00	21.64	O
ATOM	703	N	ALA	A	49	22.035	19.670	2.285	1.00	20.96	N
ATOM	705	CA	ALA	A	49	22.951	18.532	2.483	1.00	22.38	C
ATOM	707	CB	ALA	A	49	22.192	17.247	2.068	1.00	22.64	C
ATOM	711	C	ALA	A	49	24.233	18.644	1.718	1.00	23.21	C
ATOM	712	O	ALA	A	49	24.228	18.551	0.500	1.00	26.19	O
ATOM	713	N	GLU	A	50	25.328	18.866	2.426	1.00	20.40	N
ATOM	715	CA	GLU	A	50	26.598	18.826	1.753	1.00	21.76	C

ATOM	717	CB	GLU	A	50	27.625	19.892	2.250	1.00	22.32	C
ATOM	720	CG	GLU	A	50	27.374	21.244	1.591	1.00	26.62	C
ATOM	723	CD	GLU	A	50	28.046	22.421	2.279	1.00	30.59	C
ATOM	724	OE1	GLU	A	50	28.886	22.227	3.181	1.00	24.43	O
ATOM	725	OE2	GLU	A	50	27.683	23.561	1.918	1.00	35.88	O
ATOM	726	C	GLU	A	50	27.208	17.435	1.866	1.00	20.83	C
ATOM	727	O	GLU	A	50	28.257	17.188	1.220	1.00	21.81	O
ATOM	728	N	GLN	A	51	26.761	16.586	2.783	1.00	19.08	N
ATOM	730	CA	GLN	A	51	27.273	15.186	2.847	1.00	18.38	C
ATOM	732	CB	GLN	A	51	28.416	14.936	3.863	1.00	18.98	C
ATOM	735	CG	GLN	A	51	29.720	15.707	3.698	1.00	16.56	C
ATOM	738	CD	GLN	A	51	30.864	15.082	4.418	1.00	18.35	C
ATOM	739	OE1	GLN	A	51	30.728	14.001	4.993	1.00	16.59	O
ATOM	740	NE2	GLN	A	51	32.021	15.746	4.421	1.00	18.88	N
ATOM	743	C	GLN	A	51	26.048	14.303	3.122	1.00	18.15	C
ATOM	744	O	GLN	A	51	25.088	14.739	3.753	1.00	17.95	O
ATOM	745	N	CYS	A	52	26.032	13.097	2.549	1.00	19.15	N
ATOM	747	CA	CYS	A	52	24.933	12.197	2.657	1.00	19.58	C
ATOM	749	CB	CYS	A	52	23.994	12.383	1.463	1.00	20.58	C
ATOM	752	SG	CYS	A	52	22.757	11.113	1.313	1.00	23.23	S
ATOM	753	C	CYS	A	52	25.609	10.827	2.666	1.00	19.62	C
ATOM	754	O	CYS	A	52	26.112	10.376	1.630	1.00	17.75	O
ATOM	755	N	LYS	A	53	25.706	10.188	3.841	1.00	18.28	N
ATOM	757	CA	LYS	A	53	26.435	8.938	3.934	1.00	17.30	C
ATOM	759	CB	LYS	A	53	27.835	9.165	4.542	1.00	17.03	C
ATOM	762	CG	LYS	A	53	28.733	10.042	3.720	1.00	16.05	C
ATOM	765	CD	LYS	A	53	30.097	10.281	4.325	1.00	17.76	C
ATOM	768	CE	LYS	A	53	31.031	11.033	3.333	1.00	17.09	C
ATOM	771	NZ	LYS	A	53	32.138	11.733	3.893	1.00	19.33	N
ATOM	775	C	LYS	A	53	25.698	7.913	4.801	1.00	18.20	C
ATOM	776	O	LYS	A	53	24.966	8.299	5.712	1.00	15.09	O
ATOM	777	N	ASP	A	54	25.905	6.619	4.518	1.00	15.90	N
ATOM	779	CA	ASP	A	54	25.186	5.563	5.218	1.00	17.38	C
ATOM	781	CB	ASP	A	54	24.244	4.911	4.223	1.00	17.91	C
ATOM	784	CG	ASP	A	54	23.222	3.960	4.825	1.00	20.51	C
ATOM	785	OD1	ASP	A	54	23.261	3.554	6.029	1.00	15.70	O
ATOM	786	OD2	ASP	A	54	22.292	3.563	4.088	1.00	19.49	O
ATOM	787	C	ASP	A	54	26.131	4.552	5.807	1.00	17.88	C
ATOM	788	O	ASP	A	54	26.969	3.968	5.093	1.00	17.08	O
ATOM	789	N	PHE	A	55	25.998	4.356	7.135	1.00	15.74	N
ATOM	791	CA	PHE	A	55	26.865	3.464	7.867	1.00	15.03	C
ATOM	793	CB	PHE	A	55	27.359	4.168	9.131	1.00	13.99	C
ATOM	796	CG	PHE	A	55	28.268	5.336	8.844	1.00	15.45	C
ATOM	797	CD1	PHE	A	55	27.753	6.544	8.432	1.00	15.76	C
ATOM	799	CE1	PHE	A	55	28.616	7.657	8.155	1.00	14.10	C
ATOM	801	CZ	PHE	A	55	29.907	7.536	8.256	1.00	13.98	C
ATOM	803	CE2	PHE	A	55	30.431	6.303	8.656	1.00	15.61	C
ATOM	805	CD2	PHE	A	55	29.594	5.232	8.950	1.00	14.62	C
ATOM	807	C	PHE	A	55	26.160	2.191	8.265	1.00	15.07	C
ATOM	808	O	PHE	A	55	26.732	1.387	9.025	1.00	15.44	O
ATOM	809	N	THR	A	56	24.962	1.994	7.769	1.00	15.31	N
ATOM	811	CA	THR	A	56	24.149	0.858	8.159	1.00	16.77	C
ATOM	813	CB	THR	A	56	22.724	1.253	8.463	1.00	17.17	C
ATOM	815	OG1	THR	A	56	22.006	1.623	7.272	1.00	15.48	O
ATOM	817	CG2	THR	A	56	22.628	2.535	9.443	1.00	13.67	C
ATOM	821	C	THR	A	56	24.134	-0.328	7.166	1.00	20.28	C
ATOM	822	O	THR	A	56	23.451	-1.319	7.407	1.00	21.69	O
ATOM	823	N	GLN	A	57	24.852	-0.239	6.069	1.00	22.81	N

ATOM	825	CA	GLN	A	57	24.736	-1.314	5.061	1.00	25.52	C
ATOM	827	CB	GLN	A	57	24.681	-0.724	3.646	1.00	25.67	C
ATOM	830	CG	GLN	A	57	23.521	0.217	3.502	1.00	27.65	C
ATOM	833	CD	GLN	A	57	23.366	0.800	2.117	1.00	36.31	C
ATOM	834	OE1	GLN	A	57	23.871	0.240	1.156	1.00	35.97	O
ATOM	835	NE2	GLN	A	57	22.686	1.938	2.016	1.00	30.80	N
ATOM	838	C	GLN	A	57	25.848	-2.331	5.196	1.00	28.75	C
ATOM	839	O	GLN	A	57	26.735	-2.182	6.034	1.00	28.60	O
ATOM	840	N	SER	A	58	25.792	-3.388	4.363	1.00	32.27	N
ATOM	842	CA	SER	A	58	26.798	-4.440	4.371	1.00	34.96	C
ATOM	844	CB	SER	A	58	26.488	-5.494	3.291	1.00	35.23	C
ATOM	847	OG	SER	A	58	25.088	-5.548	3.041	1.00	37.60	O
ATOM	849	C	SER	A	58	28.149	-3.762	4.140	1.00	35.56	C
ATOM	850	O	SER	A	58	29.096	-3.989	4.843	1.00	36.58	O
ATOM	851	N	ASN	A	59	28.224	-2.889	3.147	1.00	37.91	N
ATOM	853	CA	ASN	A	59	29.409	-2.054	3.003	1.00	38.41	C
ATOM	855	CB	ASN	A	59	29.288	-1.232	1.739	1.00	39.92	C
ATOM	858	CG	ASN	A	59	30.172	-1.727	0.636	1.00	44.62	C
ATOM	859	OD1	ASN	A	59	31.413	-1.752	0.759	1.00	52.42	O
ATOM	860	ND2	ASN	A	59	29.547	-2.121	-0.468	1.00	50.97	N
ATOM	863	C	ASN	A	59	29.421	-1.061	4.156	1.00	37.64	C
ATOM	864	O	ASN	A	59	28.436	-0.360	4.338	1.00	37.26	O
ATOM	865	N	PRO	A	60	30.474	-1.028	4.961	1.00	37.50	N
ATOM	866	CA	PRO	A	60	30.591	-0.066	6.064	1.00	36.81	C
ATOM	868	CB	PRO	A	60	32.016	-0.315	6.585	1.00	37.80	C
ATOM	871	CG	PRO	A	60	32.661	-1.116	5.519	1.00	38.85	C
ATOM	874	CD	PRO	A	60	31.589	-1.986	4.997	1.00	38.04	C
ATOM	877	C	PRO	A	60	30.421	1.431	5.770	1.00	35.74	C
ATOM	878	O	PRO	A	60	30.266	2.188	6.749	1.00	34.22	O
ATOM	879	N	LEU	A	61	30.478	1.876	4.517	1.00	33.77	N
ATOM	881	CA	LEU	A	61	30.183	3.278	4.258	1.00	33.86	C
ATOM	883	CB	LEU	A	61	31.403	4.170	4.541	1.00	34.63	C
ATOM	886	CG	LEU	A	61	31.122	5.691	4.652	1.00	38.34	C
ATOM	888	CD1	LEU	A	61	32.418	6.454	4.765	1.00	41.14	C
ATOM	892	CD2	LEU	A	61	30.383	6.236	3.501	1.00	40.32	C
ATOM	896	C	LEU	A	61	29.681	3.440	2.838	1.00	31.90	C
ATOM	897	O	LEU	A	61	30.371	3.109	1.887	1.00	32.30	O
ATOM	898	N	VAL	A	62	28.452	3.862	2.682	1.00	29.42	N
ATOM	900	CA	VAL	A	62	27.944	4.129	1.363	1.00	29.40	C
ATOM	902	CB	VAL	A	62	26.721	3.365	1.091	1.00	28.97	C
ATOM	904	CG1	VAL	A	62	26.082	3.877	-0.187	1.00	30.81	C
ATOM	908	CG2	VAL	A	62	27.060	1.874	1.015	1.00	31.48	C
ATOM	912	C	VAL	A	62	27.768	5.625	1.255	1.00	27.76	C
ATOM	913	O	VAL	A	62	27.015	6.233	1.970	1.00	26.96	O
ATOM	914	N	ASP	A	63	28.646	6.224	0.470	1.00	28.18	N
ATOM	916	CA	ASP	A	63	28.600	7.643	0.235	1.00	26.20	C
ATOM	918	CB	ASP	A	63	29.993	8.062	-0.215	1.00	26.90	C
ATOM	921	CG	ASP	A	63	30.222	9.517	-0.099	1.00	25.49	C
ATOM	922	OD1	ASP	A	63	29.290	10.281	-0.017	1.00	26.02	O
ATOM	923	OD2	ASP	A	63	31.318	10.031	-0.150	1.00	28.08	O
ATOM	924	C	ASP	A	63	27.571	7.929	-0.826	1.00	27.79	C
ATOM	925	O	ASP	A	63	27.455	7.199	-1.812	1.00	27.28	O
ATOM	926	N	GLY	A	64	26.753	8.936	-0.581	1.00	26.48	N
ATOM	928	CA	GLY	A	64	25.703	9.316	-1.502	1.00	25.76	C
ATOM	931	C	GLY	A	64	24.357	8.742	-1.234	1.00	25.62	C
ATOM	932	O	GLY	A	64	23.474	8.881	-2.053	1.00	28.14	O
ATOM	933	N	SER	A	65	24.184	8.096	-0.080	1.00	22.83	N
ATOM	935	CA	SER	A	65	22.953	7.499	0.304	1.00	22.85	C

ATOM	937	CB	SER	A	65	23.003	6.005	0.117	1.00	23.23	C
ATOM	940	OG	SER	A	65	21.699	5.584	0.027	1.00	29.80	O
ATOM	942	C	SER	A	65	22.705	7.773	1.749	1.00	21.08	C
ATOM	943	O	SER	A	65	23.671	7.638	2.504	1.00	19.41	O
ATOM	944	N	CYS	A	66	21.521	8.181	2.140	1.00	20.00	N
ATOM	946	CA	CYS	A	66	21.278	8.539	3.546	1.00	20.11	C
ATOM	948	CB	CYS	A	66	22.034	9.822	3.885	1.00	19.63	C
ATOM	951	SG	CYS	A	66	21.484	11.254	2.900	1.00	19.95	S
ATOM	952	C	CYS	A	66	19.803	8.601	3.712	1.00	18.81	C
ATOM	953	O	CYS	A	66	19.168	9.468	4.308	1.00	17.95	O
ATOM	954	N	THR	A	67	19.180	7.568	3.214	1.00	19.39	N
ATOM	956	CA	THR	A	67	17.768	7.596	3.075	1.00	19.72	C
ATOM	958	CB	THR	A	67	17.481	6.628	1.924	1.00	20.77	C
ATOM	960	OG1	THR	A	67	18.082	7.189	0.735	1.00	26.00	O
ATOM	962	CG2	THR	A	67	16.113	6.443	1.665	1.00	23.79	C
ATOM	966	C	THR	A	67	16.941	7.325	4.315	1.00	18.14	C
ATOM	967	O	THR	A	67	17.066	6.297	4.990	1.00	16.62	O
ATOM	968	N	ASP	A	68	16.070	8.278	4.623	1.00	17.54	N
ATOM	970	CA	ASP	A	68	15.191	8.149	5.786	1.00	17.68	C
ATOM	972	CB	ASP	A	68	14.877	9.530	6.360	1.00	16.82	C
ATOM	975	CG	ASP	A	68	14.131	9.480	7.697	1.00	17.49	C
ATOM	976	OD1	ASP	A	68	13.988	8.380	8.314	1.00	14.56	O
ATOM	977	OD2	ASP	A	68	13.610	10.516	8.221	1.00	16.31	O
ATOM	978	C	ASP	A	68	13.909	7.425	5.423	1.00	19.14	C
ATOM	979	O	ASP	A	68	13.100	7.936	4.626	1.00	19.83	O
ATOM	980	N	ARG	A	69	13.688	6.262	6.023	1.00	19.38	N
ATOM	982	CA	ARG	A	69	12.427	5.549	5.858	1.00	20.20	C
ATOM	984	CB	ARG	A	69	12.665	4.106	5.357	1.00	20.57	C
ATOM	987	CG	ARG	A	69	13.461	4.061	4.081	1.00	23.84	C
ATOM	990	CD	ARG	A	69	13.499	2.688	3.401	1.00	28.11	C
ATOM	993	NE	ARG	A	69	14.384	2.688	2.239	1.00	31.97	N
ATOM	995	CZ	ARG	A	69	15.683	2.433	2.284	1.00	34.34	C
ATOM	996	NH1	ARG	A	69	16.288	2.155	3.437	1.00	33.57	N
ATOM	999	NH2	ARG	A	69	16.416	2.464	1.173	1.00	37.78	N
ATOM	1002	C	ARG	A	69	11.615	5.543	7.120	1.00	20.20	C
ATOM	1003	O	ARG	A	69	10.605	4.861	7.222	1.00	19.58	O
ATOM	1004	N	GLN	A	70	12.022	6.341	8.120	1.00	18.56	N
ATOM	1006	CA	GLN	A	70	11.359	6.330	9.404	1.00	18.67	C
ATOM	1008	CB	GLN	A	70	12.459	6.087	10.480	1.00	17.38	C
ATOM	1011	CG	GLN	A	70	11.887	5.512	11.734	1.00	24.45	C
ATOM	1014	CD	GLN	A	70	11.094	6.496	12.618	1.00	29.69	C
ATOM	1015	OE1	GLN	A	70	11.259	7.719	12.568	1.00	28.81	O
ATOM	1016	NE2	GLN	A	70	10.180	5.934	13.390	1.00	36.98	N
ATOM	1019	C	GLN	A	70	10.678	7.677	9.729	1.00	16.99	C
ATOM	1020	O	GLN	A	70	9.502	7.745	10.177	1.00	18.53	O
ATOM	1021	N	GLY	A	71	11.448	8.740	9.546	1.00	17.00	N
ATOM	1023	CA	GLY	A	71	10.936	10.086	9.792	1.00	16.91	C
ATOM	1026	C	GLY	A	71	11.766	10.862	10.826	1.00	16.73	C
ATOM	1027	O	GLY	A	71	12.023	12.040	10.683	1.00	16.08	O
ATOM	1028	N	HIS	A	72	12.190	10.148	11.848	1.00	15.53	N
ATOM	1030	CA	HIS	A	72	12.902	10.764	12.965	1.00	14.82	C
ATOM	1032	CB	HIS	A	72	13.305	9.625	13.926	1.00	14.91	C
ATOM	1035	CG	HIS	A	72	13.996	10.088	15.170	1.00	11.42	C
ATOM	1036	ND1	HIS	A	72	15.356	10.264	15.228	1.00	11.65	N
ATOM	1038	CE1	HIS	A	72	15.690	10.620	16.456	1.00	15.57	C
ATOM	1040	NE2	HIS	A	72	14.603	10.660	17.194	1.00	12.24	N
ATOM	1042	CD2	HIS	A	72	13.527	10.309	16.414	1.00	15.18	C
ATOM	1044	C	HIS	A	72	14.077	11.632	12.515	1.00	14.31	C

ATOM	1045	O	HIS	A	72	14.157	12.811	12.906	1.00	14.46	O
ATOM	1046	N	GLY	A	73	14.993	11.101	11.686	1.00	13.23	N
ATOM	1048	CA	GLY	A	73	16.140	11.851	11.227	1.00	13.67	C
ATOM	1051	C	GLY	A	73	15.743	13.097	10.452	1.00	14.47	C
ATOM	1052	O	GLY	A	73	16.388	14.147	10.556	1.00	14.58	O
ATOM	1053	N	THR	A	74	14.691	12.976	9.638	1.00	14.43	N
ATOM	1055	CA	THR	A	74	14.223	14.163	8.902	1.00	14.75	C
ATOM	1057	CB	THR	A	74	13.166	13.722	7.889	1.00	15.14	C
ATOM	1059	OG1	THR	A	74	13.832	12.851	6.979	1.00	14.14	O
ATOM	1061	CG2	THR	A	74	12.703	14.949	7.052	1.00	17.07	C
ATOM	1065	C	THR	A	74	13.672	15.256	9.779	1.00	13.89	C
ATOM	1066	O	THR	A	74	13.964	16.449	9.549	1.00	14.36	O
ATOM	1067	N	HIS	A	75	12.985	14.834	10.823	1.00	13.97	N
ATOM	1069	CA	HIS	A	75	12.345	15.653	11.803	1.00	13.53	C
ATOM	1071	CB	HIS	A	75	11.464	14.793	12.693	1.00	14.00	C
ATOM	1074	CG	HIS	A	75	10.525	15.543	13.566	1.00	13.88	C
ATOM	1075	ND1	HIS	A	75	10.923	16.209	14.706	1.00	13.19	N
ATOM	1077	CE1	HIS	A	75	9.888	16.830	15.235	1.00	15.22	C
ATOM	1079	NE2	HIS	A	75	8.826	16.616	14.465	1.00	15.33	N
ATOM	1081	CD2	HIS	A	75	9.203	15.822	13.415	1.00	14.61	C
ATOM	1083	C	HIS	A	75	13.464	16.423	12.565	1.00	14.20	C
ATOM	1084	O	HIS	A	75	13.447	17.650	12.685	1.00	11.71	O
ATOM	1085	N	VAL	A	76	14.436	15.685	13.031	1.00	13.61	N
ATOM	1087	CA	VAL	A	76	15.543	16.273	13.761	1.00	13.90	C
ATOM	1089	CB	VAL	A	76	16.471	15.117	14.276	1.00	12.59	C
ATOM	1091	CG1	VAL	A	76	17.771	15.657	14.716	1.00	13.85	C
ATOM	1095	CG2	VAL	A	76	15.788	14.354	15.381	1.00	13.36	C
ATOM	1099	C	VAL	A	76	16.280	17.319	12.925	1.00	13.76	C
ATOM	1100	O	VAL	A	76	16.549	18.419	13.362	1.00	13.81	O
ATOM	1101	N	ALA	A	77	16.598	16.976	11.693	1.00	13.31	N
ATOM	1103	CA	ALA	A	77	17.316	17.850	10.844	1.00	13.43	C
ATOM	1105	CB	ALA	A	77	17.586	17.164	9.553	1.00	12.82	C
ATOM	1109	C	ALA	A	77	16.538	19.154	10.631	1.00	13.42	C
ATOM	1110	O	ALA	A	77	17.137	20.256	10.595	1.00	16.51	O
ATOM	1111	N	GLY	A	78	15.223	19.047	10.501	1.00	13.22	N
ATOM	1113	CA	GLY	A	78	14.413	20.237	10.270	1.00	14.59	C
ATOM	1116	C	GLY	A	78	14.431	21.221	11.448	1.00	14.40	C
ATOM	1117	O	GLY	A	78	14.427	22.440	11.294	1.00	14.85	O
ATOM	1118	N	THR	A	79	14.537	20.673	12.643	1.00	12.64	N
ATOM	1120	CA	THR	A	79	14.546	21.535	13.817	1.00	11.83	C
ATOM	1122	CB	THR	A	79	14.350	20.656	15.063	1.00	11.71	C
ATOM	1124	OG1	THR	A	79	12.990	20.162	15.166	1.00	12.60	O
ATOM	1126	CG2	THR	A	79	14.569	21.491	16.347	1.00	11.10	C
ATOM	1130	C	THR	A	79	15.842	22.248	13.795	1.00	12.20	C
ATOM	1131	O	THR	A	79	15.917	23.440	14.122	1.00	12.14	O
ATOM	1132	N	VAL	A	80	16.917	21.568	13.358	1.00	11.44	N
ATOM	1134	CA	VAL	A	80	18.195	22.225	13.293	1.00	11.80	C
ATOM	1136	CB	VAL	A	80	19.299	21.273	12.865	1.00	11.91	C
ATOM	1138	CG1	VAL	A	80	20.637	21.963	12.687	1.00	13.34	C
ATOM	1142	CG2	VAL	A	80	19.520	20.158	13.884	1.00	12.77	C
ATOM	1146	C	VAL	A	80	18.216	23.369	12.266	1.00	13.39	C
ATOM	1147	O	VAL	A	80	18.646	24.514	12.553	1.00	12.65	O
ATOM	1148	N	LEU	A	81	17.751	23.054	11.069	1.00	13.69	N
ATOM	1150	CA	LEU	A	81	18.057	23.946	9.965	1.00	14.13	C
ATOM	1152	CB	LEU	A	81	19.454	23.675	9.439	1.00	14.13	C
ATOM	1155	CG	LEU	A	81	19.893	22.189	9.225	1.00	11.54	C
ATOM	1157	CD1	LEU	A	81	19.058	21.552	8.105	1.00	15.65	C
ATOM	1161	CD2	LEU	A	81	21.308	22.059	8.854	1.00	14.83	C

ATOM	1165	C	LEU	A	81	17.043	24.065	8.827	1.00	15.14	C
ATOM	1166	O	LEU	A	81	17.442	24.518	7.766	1.00	17.76	O
ATOM	1167	N	ALA	A	82	15.791	23.694	9.035	1.00	15.38	N
ATOM	1169	CA	ALA	A	82	14.830	23.894	7.920	1.00	16.54	C
ATOM	1171	CB	ALA	A	82	13.485	23.412	8.253	1.00	16.56	C
ATOM	1175	C	ALA	A	82	14.807	25.381	7.616	1.00	17.73	C
ATOM	1176	O	ALA	A	82	14.873	26.246	8.522	1.00	16.11	O
ATOM	1177	N	HIS	A	83	14.637	25.678	6.321	1.00	18.61	N
ATOM	1179	CA	HIS	A	83	14.802	27.048	5.845	1.00	17.82	C
ATOM	1181	CB	HIS	A	83	16.057	27.116	4.996	1.00	18.66	C
ATOM	1184	CG	HIS	A	83	16.040	26.187	3.831	1.00	19.55	C
ATOM	1185	ND1	HIS	A	83	14.935	26.066	3.023	1.00	23.39	N
ATOM	1187	CE1	HIS	A	83	15.196	25.205	2.056	1.00	24.12	C
ATOM	1189	NE2	HIS	A	83	16.395	24.706	2.259	1.00	24.21	N
ATOM	1191	CD2	HIS	A	83	16.960	25.326	3.349	1.00	22.73	C
ATOM	1193	C	HIS	A	83	13.606	27.689	5.119	1.00	19.24	C
ATOM	1194	O	HIS	A	83	13.802	28.694	4.468	1.00	20.21	O
ATOM	1195	N	GLY	A	84	12.433	27.158	5.342	1.00	19.88	N
ATOM	1197	CA	GLY	A	84	11.151	27.653	4.874	1.00	23.01	C
ATOM	1200	C	GLY	A	84	10.891	27.373	3.388	1.00	23.83	C
ATOM	1201	O	GLY	A	84	9.816	27.693	2.873	1.00	25.88	O
ATOM	1202	N	GLY	A	85	11.891	26.852	2.716	1.00	25.14	N
ATOM	1204	CA	GLY	A	85	11.754	26.452	1.333	1.00	28.31	C
ATOM	1207	C	GLY	A	85	11.845	27.607	0.361	1.00	30.82	C
ATOM	1208	O	GLY	A	85	11.704	28.777	0.750	1.00	32.32	O
ATOM	1209	N	SER	A	86	12.066	27.253	-0.910	1.00	33.23	N
ATOM	1211	CA	SER	A	86	12.332	28.220	-1.982	1.00	35.37	C
ATOM	1213	CB	SER	A	86	12.287	27.551	-3.374	1.00	35.51	C
ATOM	1216	OG	SER	A	86	11.022	26.920	-3.531	1.00	36.16	O
ATOM	1218	C	SER	A	86	11.323	29.323	-1.984	1.00	35.85	C
ATOM	1219	O	SER	A	86	11.673	30.481	-2.155	1.00	37.71	O
ATOM	1220	N	ASN	A	87	10.066	28.993	-1.784	1.00	36.18	N
ATOM	1222	CA	ASN	A	87	9.060	30.024	-1.844	1.00	37.05	C
ATOM	1224	CB	ASN	A	87	7.842	29.472	-2.589	1.00	37.33	C
ATOM	1227	CG	ASN	A	87	6.943	28.626	-1.702	1.00	40.53	C
ATOM	1228	OD1	ASN	A	87	7.323	28.240	-0.581	1.00	40.83	O
ATOM	1229	ND2	ASN	A	87	5.732	28.329	-2.205	1.00	39.22	N
ATOM	1232	C	ASN	A	87	8.678	30.600	-0.469	1.00	35.97	C
ATOM	1233	O	ASN	A	87	7.564	31.143	-0.295	1.00	36.81	O
ATOM	1234	N	GLY	A	88	9.554	30.402	0.526	1.00	34.13	N
ATOM	1236	CA	GLY	A	88	9.307	30.979	1.841	1.00	32.36	C
ATOM	1239	C	GLY	A	88	8.149	30.556	2.701	1.00	30.27	C
ATOM	1240	O	GLY	A	88	7.882	31.189	3.728	1.00	30.72	O
ATOM	1241	N	GLN	A	89	7.375	29.545	2.305	1.00	28.00	N
ATOM	1243	CA	GLN	A	89	6.212	29.190	3.117	1.00	27.11	C
ATOM	1245	CB	GLN	A	89	4.898	29.091	2.269	1.00	28.51	C
ATOM	1248	CG	GLN	A	89	3.596	28.969	3.114	0.10	26.48	C
ATOM	1251	CD	GLN	A	89	2.269	28.881	2.318	0.10	25.84	C
ATOM	1252	OE1	GLN	A	89	2.243	28.873	1.085	0.10	20.77	O
ATOM	1253	NE2	GLN	A	89	1.164	28.811	3.052	0.10	23.86	N
ATOM	1256	C	GLN	A	89	6.384	27.908	3.974	1.00	26.64	C
ATOM	1257	O	GLN	A	89	5.463	27.490	4.638	1.00	25.73	O
ATOM	1258	N	GLY	A	90	7.572	27.312	3.967	1.00	26.19	N
ATOM	1260	CA	GLY	A	90	7.781	26.104	4.760	1.00	24.89	C
ATOM	1263	C	GLY	A	90	8.133	26.372	6.223	1.00	25.02	C
ATOM	1264	O	GLY	A	90	7.940	27.492	6.751	1.00	25.06	O
ATOM	1265	N	VAL	A	91	8.598	25.330	6.888	1.00	22.83	N
ATOM	1267	CA	VAL	A	91	8.942	25.462	8.304	1.00	20.77	C

ATOM	1269	CB	VAL	A	91	8.681	24.116	9.045	1.00	19.91	C
ATOM	1271	CG1	VAL	A	91	9.781	23.160	8.797	1.00	21.25	C
ATOM	1275	CG2	VAL	A	91	8.463	24.309	10.528	1.00	21.36	C
ATOM	1279	C	VAL	A	91	10.344	25.938	8.411	1.00	18.60	C
ATOM	1280	O	VAL	A	91	11.184	25.738	7.532	1.00	19.96	O
ATOM	1281	N	TYR	A	92	10.632	26.589	9.547	1.00	18.11	N
ATOM	1283	CA	TYR	A	92	11.941	27.076	9.868	1.00	17.39	C
ATOM	1285	CB	TYR	A	92	11.880	28.546	10.256	1.00	16.87	C
ATOM	1288	CG	TYR	A	92	11.827	29.420	9.027	1.00	17.86	C
ATOM	1289	CD1	TYR	A	92	12.989	29.758	8.379	1.00	16.53	C
ATOM	1291	CE1	TYR	A	92	12.993	30.516	7.233	1.00	20.55	C
ATOM	1293	CZ	TYR	A	92	11.793	30.963	6.717	1.00	23.54	C
ATOM	1294	OH	TYR	A	92	11.862	31.737	5.549	1.00	25.77	O
ATOM	1296	CE2	TYR	A	92	10.619	30.672	7.325	1.00	19.89	C
ATOM	1298	CD2	TYR	A	92	10.626	29.840	8.507	1.00	20.04	C
ATOM	1300	C	TYR	A	92	12.542	26.375	11.099	1.00	14.56	C
ATOM	1301	O	TYR	A	92	11.856	26.154	12.042	1.00	14.48	O
ATOM	1302	N	GLY	A	93	13.824	26.133	11.058	1.00	13.49	N
ATOM	1304	CA	GLY	A	93	14.547	25.546	12.182	1.00	15.74	C
ATOM	1307	C	GLY	A	93	15.350	26.635	12.819	1.00	14.86	C
ATOM	1308	O	GLY	A	93	15.203	27.819	12.473	1.00	17.02	O
ATOM	1309	N	VAL	A	94	16.231	26.278	13.759	1.00	14.32	N
ATOM	1311	CA	VAL	A	94	16.981	27.306	14.421	1.00	14.34	C
ATOM	1313	CB	VAL	A	94	17.654	26.753	15.712	1.00	13.59	C
ATOM	1315	CG1	VAL	A	94	18.263	27.876	16.515	1.00	13.33	C
ATOM	1319	CG2	VAL	A	94	16.633	26.043	16.538	1.00	13.90	C
ATOM	1323	C	VAL	A	94	18.010	28.055	13.577	1.00	14.53	C
ATOM	1324	O	VAL	A	94	18.196	29.258	13.779	1.00	16.71	O
ATOM	1325	N	ALA	A	95	18.724	27.356	12.692	1.00	14.24	N
ATOM	1327	CA	ALA	A	95	19.859	27.839	11.990	1.00	14.00	C
ATOM	1329	CB	ALA	A	95	21.100	27.227	12.574	1.00	14.43	C
ATOM	1333	C	ALA	A	95	19.757	27.491	10.498	1.00	15.52	C
ATOM	1334	O	ALA	A	95	20.476	26.644	9.954	1.00	13.66	O
ATOM	1335	N	PRO	A	96	18.847	28.184	9.840	1.00	15.59	N
ATOM	1336	CA	PRO	A	96	18.487	27.876	8.443	1.00	16.93	C
ATOM	1338	CB	PRO	A	96	17.330	28.851	8.170	1.00	17.23	C
ATOM	1341	CG	PRO	A	96	17.628	29.986	9.086	1.00	16.22	C
ATOM	1344	CD	PRO	A	96	18.078	29.307	10.383	1.00	13.71	C
ATOM	1347	C	PRO	A	96	19.598	28.049	7.403	1.00	17.82	C
ATOM	1348	O	PRO	A	96	19.478	27.477	6.306	1.00	16.77	O
ATOM	1349	N	GLN	A	97	20.664	28.772	7.719	1.00	17.73	N
ATOM	1351	CA	GLN	A	97	21.812	28.891	6.826	1.00	18.02	C
ATOM	1353	CB	GLN	A	97	22.374	30.341	6.726	1.00	18.03	C
ATOM	1356	CG	GLN	A	97	21.509	31.218	5.783	1.00	22.97	C
ATOM	1359	CD	GLN	A	97	20.220	31.715	6.401	1.00	23.17	C
ATOM	1360	OE1	GLN	A	97	20.303	32.467	7.345	1.00	27.41	O
ATOM	1361	NE2	GLN	A	97	19.016	31.311	5.865	1.00	26.08	N
ATOM	1364	C	GLN	A	97	22.901	27.903	7.080	1.00	17.35	C
ATOM	1365	O	GLN	A	97	23.900	27.913	6.351	1.00	17.54	O
ATOM	1366	N	ALA	A	98	22.763	27.057	8.125	1.00	15.56	N
ATOM	1368	CA	ALA	A	98	23.794	26.040	8.361	1.00	16.07	C
ATOM	1370	CB	ALA	A	98	23.615	25.387	9.738	1.00	15.36	C
ATOM	1374	C	ALA	A	98	23.657	24.997	7.256	1.00	15.80	C
ATOM	1375	O	ALA	A	98	22.610	24.906	6.610	1.00	18.34	O
ATOM	1376	N	LYS	A	99	24.683	24.195	7.082	1.00	16.19	N
ATOM	1378	CA	LYS	A	99	24.670	23.108	6.118	1.00	15.45	C
ATOM	1380	CB	LYS	A	99	25.882	23.152	5.268	1.00	16.64	C
ATOM	1383	CG	LYS	A	99	25.789	24.264	4.222	1.00	17.86	C

ATOM	1386	CD	LYS	A	99	24.616	24.101	3.322	1.00	22.94	C
ATOM	1389	CE	LYS	A	99	24.844	25.062	2.185	1.00	28.36	C
ATOM	1392	NZ	LYS	A	99	23.614	25.181	1.383	1.00	28.94	N
ATOM	1396	C	LYS	A	99	24.604	21.759	6.887	1.00	15.54	C
ATOM	1397	O	LYS	A	99	25.012	21.684	8.019	1.00	15.10	O
ATOM	1398	N	LEU	A	100	24.136	20.742	6.185	1.00	14.73	N
ATOM	1400	CA	LEU	A	100	23.801	19.460	6.791	1.00	15.28	C
ATOM	1402	CB	LEU	A	100	22.361	19.131	6.489	1.00	14.80	C
ATOM	1405	CG	LEU	A	100	21.852	17.724	6.719	1.00	16.65	C
ATOM	1407	CD1	LEU	A	100	21.751	17.484	8.242	1.00	17.43	C
ATOM	1411	CD2	LEU	A	100	20.500	17.473	6.155	1.00	17.01	C
ATOM	1415	C	LEU	A	100	24.743	18.373	6.336	1.00	15.64	C
ATOM	1416	O	LEU	A	100	25.114	18.290	5.154	1.00	17.60	O
ATOM	1417	N	TRP	A	101	25.206	17.566	7.298	1.00	15.09	N
ATOM	1419	CA	TRP	A	101	25.895	16.350	6.942	1.00	15.10	C
ATOM	1421	CB	TRP	A	101	27.265	16.234	7.534	1.00	14.66	C
ATOM	1424	CG	TRP	A	101	28.408	17.171	7.076	1.00	13.68	C
ATOM	1425	CD1	TRP	A	101	28.342	18.164	6.137	1.00	14.24	C
ATOM	1427	NE1	TRP	A	101	29.575	18.741	5.956	1.00	14.73	N
ATOM	1429	CE2	TRP	A	101	30.465	18.110	6.770	1.00	14.20	C
ATOM	1430	CD2	TRP	A	101	29.751	17.123	7.498	1.00	15.01	C
ATOM	1431	CE3	TRP	A	101	30.470	16.329	8.413	1.00	15.44	C
ATOM	1433	CZ3	TRP	A	101	31.791	16.598	8.605	1.00	14.31	C
ATOM	1435	CH2	TRP	A	101	32.451	17.587	7.845	1.00	15.17	C
ATOM	1437	CZ2	TRP	A	101	31.780	18.363	6.977	1.00	14.09	C
ATOM	1439	C	TRP	A	101	24.932	15.267	7.451	1.00	16.46	C
ATOM	1440	O	TRP	A	101	24.830	15.022	8.675	1.00	14.81	O
ATOM	1441	N	ALA	A	102	24.250	14.579	6.534	1.00	14.78	N
ATOM	1443	CA	ALA	A	102	23.255	13.610	6.910	1.00	15.54	C
ATOM	1445	CB	ALA	A	102	22.086	13.639	5.973	1.00	16.18	C
ATOM	1449	C	ALA	A	102	23.897	12.221	6.941	1.00	15.83	C
ATOM	1450	O	ALA	A	102	24.187	11.661	5.898	1.00	15.17	O
ATOM	1451	N	TYR	A	103	24.148	11.692	8.140	1.00	14.35	N
ATOM	1453	CA	TYR	A	103	24.797	10.400	8.290	1.00	14.35	C
ATOM	1455	CB	TYR	A	103	25.985	10.493	9.225	1.00	13.92	C
ATOM	1458	CG	TYR	A	103	27.247	11.147	8.697	1.00	13.29	C
ATOM	1459	CD1	TYR	A	103	27.275	11.938	7.550	1.00	14.70	C
ATOM	1461	CE1	TYR	A	103	28.455	12.512	7.113	1.00	14.99	C
ATOM	1463	CZ	TYR	A	103	29.587	12.335	7.783	1.00	13.42	C
ATOM	1464	OH	TYR	A	103	30.820	12.886	7.417	1.00	17.55	O
ATOM	1466	CE2	TYR	A	103	29.608	11.561	8.961	1.00	11.55	C
ATOM	1468	CD2	TYR	A	103	28.445	10.996	9.399	1.00	12.45	C
ATOM	1470	C	TYR	A	103	23.813	9.419	8.860	1.00	13.70	C
ATOM	1471	O	TYR	A	103	23.336	9.583	9.966	1.00	13.01	O
ATOM	1472	N	LYS	A	104	23.490	8.383	8.101	1.00	13.67	N
ATOM	1474	CA	LYS	A	104	22.524	7.385	8.564	1.00	12.46	C
ATOM	1476	CB	LYS	A	104	21.773	6.738	7.407	1.00	14.90	C
ATOM	1479	CG	LYS	A	104	20.789	5.718	7.815	1.00	15.07	C
ATOM	1482	CD	LYS	A	104	19.991	5.144	6.616	1.00	14.19	C
ATOM	1485	CE	LYS	A	104	18.751	4.402	7.036	1.00	17.35	C
ATOM	1488	NZ	LYS	A	104	18.027	3.784	5.831	1.00	15.18	N
ATOM	1492	C	LYS	A	104	23.249	6.327	9.362	1.00	14.29	C
ATOM	1493	O	LYS	A	104	24.138	5.652	8.836	1.00	14.08	O
ATOM	1494	N	VAL	A	105	22.893	6.215	10.645	1.00	12.75	N
ATOM	1496	CA	VAL	A	105	23.513	5.287	11.592	1.00	13.70	C
ATOM	1498	CB	VAL	A	105	24.301	6.043	12.684	1.00	13.12	C
ATOM	1500	CG1	VAL	A	105	25.244	6.961	12.010	1.00	14.29	C
ATOM	1504	CG2	VAL	A	105	23.388	6.804	13.578	1.00	12.47	C

ATOM	1508	C	VAL	A	105	22.491	4.405	12.292	1.00	13.35	C
ATOM	1509	O	VAL	A	105	22.851	3.501	13.036	1.00	14.40	O
ATOM	1510	N	LEU	A	106	21.218	4.733	12.140	1.00	13.80	N
ATOM	1512	CA	LEU	A	106	20.133	3.912	12.678	1.00	15.31	C
ATOM	1514	CB	LEU	A	106	19.165	4.715	13.533	1.00	14.78	C
ATOM	1517	CG	LEU	A	106	19.820	5.395	14.752	1.00	14.84	C
ATOM	1519	CD1	LEU	A	106	18.745	6.216	15.434	1.00	13.44	C
ATOM	1523	CD2	LEU	A	106	20.365	4.281	15.645	1.00	13.80	C
ATOM	1527	C	LEU	A	106	19.328	3.395	11.488	1.00	16.71	C
ATOM	1528	O	LEU	A	106	19.217	4.083	10.457	1.00	14.73	O
ATOM	1529	N	GLY	A	107	18.812	2.184	11.617	1.00	18.94	N
ATOM	1531	CA	GLY	A	107	17.950	1.629	10.581	1.00	20.89	C
ATOM	1534	C	GLY	A	107	16.534	2.176	10.597	1.00	22.18	C
ATOM	1535	O	GLY	A	107	16.136	3.087	11.335	1.00	21.65	O
ATOM	1536	N	ASP	A	108	15.714	1.570	9.755	1.00	24.79	N
ATOM	1538	CA	ASP	A	108	14.419	2.139	9.442	1.00	25.79	C
ATOM	1540	CB	ASP	A	108	13.946	1.584	8.117	1.00	26.09	C
ATOM	1543	CG	ASP	A	108	14.971	1.774	7.022	1.00	28.51	C
ATOM	1544	OD1	ASP	A	108	15.795	2.721	7.082	1.00	27.80	O
ATOM	1545	OD2	ASP	A	108	15.020	1.038	6.025	1.00	30.77	O
ATOM	1546	C	ASP	A	108	13.331	1.997	10.489	1.00	26.41	C
ATOM	1547	O	ASP	A	108	12.229	2.535	10.294	1.00	26.78	O
ATOM	1548	N	ASN	A	109	13.629	1.262	11.566	1.00	26.19	N
ATOM	1550	CA	ASN	A	109	12.751	1.172	12.719	1.00	25.53	C
ATOM	1552	CB	ASN	A	109	12.399	-0.264	13.022	1.00	26.84	C
ATOM	1555	CG	ASN	A	109	11.599	-0.920	11.863	1.00	30.82	C
ATOM	1556	OD1	ASN	A	109	10.606	-0.338	11.353	1.00	35.24	O
ATOM	1557	ND2	ASN	A	109	12.038	-2.093	11.429	1.00	36.51	N
ATOM	1560	C	ASN	A	109	13.340	1.943	13.933	1.00	24.23	C
ATOM	1561	O	ASN	A	109	12.941	1.773	15.071	1.00	23.68	O
ATOM	1562	N	GLY	A	110	14.325	2.774	13.652	1.00	22.01	N
ATOM	1564	CA	GLY	A	110	14.823	3.684	14.685	1.00	20.58	C
ATOM	1567	C	GLY	A	110	15.783	3.001	15.656	1.00	18.79	C
ATOM	1568	O	GLY	A	110	15.989	3.492	16.797	1.00	18.63	O
ATOM	1569	N	SER	A	111	16.373	1.885	15.208	1.00	16.52	N
ATOM	1571	CA	SER	A	111	17.377	1.225	16.057	1.00	17.48	C
ATOM	1573	CB	SER	A	111	16.805	0.002	16.752	1.00	18.93	C
ATOM	1576	OG	SER	A	111	16.663	-1.046	15.856	1.00	20.57	O
ATOM	1578	C	SER	A	111	18.625	0.916	15.250	1.00	15.84	C
ATOM	1579	O	SER	A	111	18.585	0.814	14.022	1.00	15.08	O
ATOM	1580	N	GLY	A	112	19.767	0.761	15.913	1.00	15.46	N
ATOM	1582	CA	GLY	A	112	20.991	0.537	15.198	1.00	14.74	C
ATOM	1585	C	GLY	A	112	22.080	-0.033	16.063	1.00	13.99	C
ATOM	1586	O	GLY	A	112	21.852	-0.365	17.219	1.00	12.44	O
ATOM	1587	N	TYR	A	113	23.229	-0.171	15.431	1.00	13.65	N
ATOM	1589	CA	TYR	A	113	24.372	-0.836	16.000	1.00	14.69	C
ATOM	1591	CB	TYR	A	113	24.992	-1.754	14.982	1.00	14.83	C
ATOM	1594	CG	TYR	A	113	24.139	-2.928	14.627	1.00	16.70	C
ATOM	1595	CD1	TYR	A	113	24.217	-4.098	15.339	1.00	18.38	C
ATOM	1597	CE1	TYR	A	113	23.392	-5.213	14.997	1.00	18.28	C
ATOM	1599	CZ	TYR	A	113	22.516	-5.121	13.926	1.00	19.64	C
ATOM	1600	OH	TYR	A	113	21.730	-6.214	13.573	1.00	20.11	O
ATOM	1602	CE2	TYR	A	113	22.465	-3.958	13.189	1.00	19.66	C
ATOM	1604	CD2	TYR	A	113	23.269	-2.871	13.557	1.00	15.59	C
ATOM	1606	C	TYR	A	113	25.441	0.094	16.471	1.00	13.86	C
ATOM	1607	O	TYR	A	113	25.825	1.019	15.758	1.00	14.60	O
ATOM	1608	N	SER	A	114	25.880	-0.113	17.706	1.00	13.30	N
ATOM	1610	CA	SER	A	114	26.958	0.655	18.290	1.00	13.35	C

ATOM	1612	CB	SER	A	114	27.507	-0.213	19.432	1.00	15.78	C
ATOM	1615	OG	SER	A	114	28.722	0.270	19.995	1.00	14.15	O
ATOM	1617	C	SER	A	114	28.125	0.916	17.339	1.00	14.05	C
ATOM	1618	O	SER	A	114	28.615	2.023	17.226	1.00	13.89	O
ATOM	1619	N	ASP	A	115	28.581	-0.139	16.665	1.00	13.29	N
ATOM	1621	CA	ASP	A	115	29.724	0.014	15.754	1.00	14.72	C
ATOM	1623	CB	AASP	A	115	30.159	-1.299	15.125	0.50	16.85	C
ATOM	1624	CB	BASP	A	115	29.949	-1.288	14.969	0.50	15.71	C
ATOM	1629	CG	AASP	A	115	29.100	-1.900	14.308	0.50	20.25	C
ATOM	1630	CG	BASP	A	115	30.701	-2.324	15.752	0.50	16.91	C
ATOM	1631	OD1	AASP	A	115	28.555	-1.177	13.460	0.50	32.11	O
ATOM	1632	OD1	BASP	A	115	31.693	-1.951	16.379	0.50	24.07	O
ATOM	1633	OD2	AASP	A	115	28.717	-3.057	14.477	0.50	33.25	O
ATOM	1634	OD2	BASP	A	115	30.401	-3.501	15.764	0.50	20.69	O
ATOM	1635	C	ASP	A	115	29.511	1.034	14.682	1.00	13.31	C
ATOM	1636	O	ASP	A	115	30.488	1.671	14.268	1.00	13.00	O
ATOM	1637	N	ASP	A	116	28.292	1.098	14.156	1.00	12.95	N
ATOM	1639	CA	ASP	A	116	27.982	1.996	13.046	1.00	13.15	C
ATOM	1641	CB	ASP	A	116	26.618	1.685	12.446	1.00	14.36	C
ATOM	1644	CG	ASP	A	116	26.506	0.299	11.819	1.00	14.39	C
ATOM	1645	OD1	ASP	A	116	27.509	-0.378	11.592	1.00	13.15	O
ATOM	1646	OD2	ASP	A	116	25.408	-0.179	11.584	1.00	13.28	O
ATOM	1647	C	ASP	A	116	28.001	3.437	13.581	1.00	13.01	C
ATOM	1648	O	ASP	A	116	28.529	4.354	12.937	1.00	13.99	O
ATOM	1649	N	ILE	A	117	27.409	3.644	14.748	1.00	13.05	N
ATOM	1651	CA	ILE	A	117	27.404	4.952	15.339	1.00	12.04	C
ATOM	1653	CB	ILE	A	117	26.518	4.961	16.572	1.00	12.89	C
ATOM	1655	CG1	ILE	A	117	25.034	4.744	16.168	1.00	17.41	C
ATOM	1658	CD1	ILE	A	117	24.279	3.948	17.085	1.00	21.55	C
ATOM	1662	CG2	ILE	A	117	26.715	6.288	17.378	1.00	15.14	C
ATOM	1666	C	ILE	A	117	28.813	5.403	15.623	1.00	11.86	C
ATOM	1667	O	ILE	A	117	29.195	6.548	15.321	1.00	12.61	O
ATOM	1668	N	ALA	A	118	29.609	4.532	16.227	1.00	10.45	N
ATOM	1670	CA	ALA	A	118	30.981	4.891	16.519	1.00	11.56	C
ATOM	1672	CB	ALA	A	118	31.649	3.800	17.353	1.00	11.97	C
ATOM	1676	C	ALA	A	118	31.786	5.248	15.273	1.00	11.35	C
ATOM	1677	O	ALA	A	118	32.511	6.241	15.232	1.00	10.56	O
ATOM	1678	N	ALA	A	119	31.597	4.459	14.253	1.00	11.09	N
ATOM	1680	CA	ALA	A	119	32.298	4.693	13.010	1.00	10.91	C
ATOM	1682	CB	ALA	A	119	32.030	3.600	12.104	1.00	11.91	C
ATOM	1686	C	ALA	A	119	31.875	6.029	12.430	1.00	10.50	C
ATOM	1687	O	ALA	A	119	32.721	6.808	11.942	1.00	12.46	O
ATOM	1688	N	ALA	A	120	30.589	6.342	12.539	1.00	11.95	N
ATOM	1690	CA	ALA	A	120	30.079	7.579	12.001	1.00	11.18	C
ATOM	1692	CB	ALA	A	120	28.626	7.575	12.034	1.00	11.63	C
ATOM	1696	C	ALA	A	120	30.643	8.813	12.743	1.00	11.63	C
ATOM	1697	O	ALA	A	120	31.033	9.799	12.104	1.00	11.85	O
ATOM	1698	N	ILE	A	121	30.708	8.753	14.070	1.00	10.33	N
ATOM	1700	CA	ILE	A	121	31.291	9.848	14.892	1.00	10.58	C
ATOM	1702	CB	ILE	A	121	31.215	9.481	16.379	1.00	11.12	C
ATOM	1704	CG1	ILE	A	121	29.768	9.320	16.750	1.00	11.01	C
ATOM	1707	CD1	ILE	A	121	29.566	8.668	18.128	1.00	11.36	C
ATOM	1711	CG2	ILE	A	121	31.860	10.543	17.229	1.00	12.83	C
ATOM	1715	C	ILE	A	121	32.749	10.129	14.510	1.00	11.68	C
ATOM	1716	O	ILE	A	121	33.158	11.259	14.287	1.00	12.00	O
ATOM	1717	N	ARG	A	122	33.536	9.055	14.448	1.00	11.70	N
ATOM	1719	CA	ARG	A	122	34.929	9.171	14.046	1.00	13.86	C
ATOM	1721	CB	ARG	A	122	35.603	7.810	14.114	1.00	14.57	C

ATOM	1724	CG	ARG	A	122	35.715	7.320	15.531	1.00	14.77	C
ATOM	1727	CD	ARG	A	122	36.384	5.975	15.679	1.00	18.79	C
ATOM	1730	NE	ARG	A	122	36.784	5.757	17.048	1.00	21.92	N
ATOM	1732	CZ	ARG	A	122	37.945	6.112	17.577	1.00	22.62	C
ATOM	1733	NH1	ARG	A	122	38.894	6.640	16.838	1.00	20.73	N
ATOM	1736	NH2	ARG	A	122	38.178	5.850	18.857	1.00	29.11	N
ATOM	1739	C	ARG	A	122	35.088	9.760	12.636	1.00	14.45	C
ATOM	1740	O	ARG	A	122	35.992	10.563	12.389	1.00	13.33	O
ATOM	1741	N	HIS	A	123	34.198	9.348	11.743	1.00	12.96	N
ATOM	1743	CA	HIS	A	123	34.231	9.828	10.385	1.00	14.40	C
ATOM	1745	CB	HIS	A	123	33.324	9.001	9.522	1.00	14.46	C
ATOM	1748	CG	HIS	A	123	33.390	9.347	8.065	1.00	17.57	C
ATOM	1749	ND1	HIS	A	123	34.358	8.843	7.224	1.00	26.34	N
ATOM	1751	CE1	HIS	A	123	34.183	9.333	6.005	1.00	26.65	C
ATOM	1753	NE2	HIS	A	123	33.120	10.115	6.015	1.00	23.02	N
ATOM	1755	CD2	HIS	A	123	32.596	10.125	7.299	1.00	22.31	C
ATOM	1757	C	HIS	A	123	33.913	11.345	10.332	1.00	15.58	C
ATOM	1758	O	HIS	A	123	34.587	12.095	9.658	1.00	14.13	O
ATOM	1759	N	VAL	A	124	32.914	11.801	11.081	1.00	13.58	N
ATOM	1761	CA	VAL	A	124	32.701	13.233	11.195	1.00	13.94	C
ATOM	1763	CB	VAL	A	124	31.583	13.598	12.235	1.00	13.67	C
ATOM	1765	CG1	VAL	A	124	31.476	15.111	12.408	1.00	11.98	C
ATOM	1769	CG2	VAL	A	124	30.258	13.019	11.847	1.00	14.52	C
ATOM	1773	C	VAL	A	124	33.980	13.971	11.580	1.00	12.11	C
ATOM	1774	O	VAL	A	124	34.323	14.973	10.938	1.00	13.19	O
ATOM	1775	N	ALA	A	125	34.672	13.495	12.604	1.00	12.61	N
ATOM	1777	CA	ALA	A	125	35.875	14.123	13.121	1.00	12.03	C
ATOM	1779	CB	ALA	A	125	36.351	13.398	14.322	1.00	11.98	C
ATOM	1783	C	ALA	A	125	36.972	14.158	12.062	1.00	13.52	C
ATOM	1784	O	ALA	A	125	37.610	15.186	11.838	1.00	13.20	O
ATOM	1785	N	ASP	A	126	37.081	13.059	11.312	1.00	13.79	N
ATOM	1787	CA	ASP	A	126	38.087	12.980	10.268	1.00	15.94	C
ATOM	1789	CB	ASP	A	126	38.180	11.566	9.743	1.00	16.11	C
ATOM	1792	CG	ASP	A	126	38.895	10.635	10.677	1.00	16.70	C
ATOM	1793	OD1	ASP	A	126	39.620	11.075	11.580	1.00	17.85	O
ATOM	1794	OD2	ASP	A	126	38.795	9.393	10.586	1.00	17.09	O
ATOM	1795	C	ASP	A	126	37.736	13.933	9.133	1.00	16.71	C
ATOM	1796	O	ASP	A	126	38.604	14.612	8.602	1.00	17.22	O
ATOM	1797	N	GLU	A	127	36.465	14.027	8.798	1.00	16.48	N
ATOM	1799	CA	GLU	A	127	36.033	14.934	7.759	1.00	17.08	C
ATOM	1801	CB	GLU	A	127	34.580	14.723	7.386	1.00	17.14	C
ATOM	1804	CG	GLU	A	127	34.319	13.431	6.618	1.00	18.23	C
ATOM	1807	CD	GLU	A	127	34.875	13.485	5.205	1.00	23.17	C
ATOM	1808	OE1	GLU	A	127	34.333	14.250	4.412	1.00	22.57	O
ATOM	1809	OE2	GLU	A	127	35.887	12.809	4.967	1.00	25.80	O
ATOM	1810	C	GLU	A	127	36.256	16.370	8.204	1.00	18.24	C
ATOM	1811	O	GLU	A	127	36.634	17.255	7.393	1.00	17.10	O
ATOM	1812	N	ALA	A	128	35.969	16.626	9.465	1.00	16.20	N
ATOM	1814	CA	ALA	A	128	36.165	17.979	10.000	1.00	17.01	C
ATOM	1816	CB	ALA	A	128	35.582	18.100	11.469	1.00	18.11	C
ATOM	1820	C	ALA	A	128	37.607	18.403	9.959	1.00	17.06	C
ATOM	1821	O	ALA	A	128	37.923	19.537	9.561	1.00	18.46	O
ATOM	1822	N	SER	A	129	38.496	17.519	10.360	1.00	17.73	N
ATOM	1824	CA	SER	A	129	39.896	17.869	10.334	1.00	19.04	C
ATOM	1826	CB	SER	A	129	40.735	16.796	10.996	1.00	19.88	C
ATOM	1829	OG	SER	A	129	40.289	15.493	10.649	1.00	28.54	O
ATOM	1831	C	SER	A	129	40.367	18.063	8.907	1.00	18.31	C
ATOM	1832	O	SER	A	129	41.158	18.968	8.641	1.00	19.92	O

ATOM	1833	N	ARG	A	130	39.927	17.209	8.003	1.00	17.50	N
ATOM	1835	CA	ARG	A	130	40.418	17.258	6.611	1.00	17.79	C
ATOM	1837	CB	ARG	A	130	39.938	16.052	5.802	1.00	17.78	C
ATOM	1840	CG	ARG	A	130	40.573	15.989	4.406	1.00	17.70	C
ATOM	1843	CD	ARG	A	130	40.048	14.864	3.632	1.00	18.82	C
ATOM	1846	NE	ARG	A	130	38.768	15.271	3.064	1.00	25.15	N
ATOM	1848	CZ	ARG	A	130	37.641	14.760	3.393	1.00	25.02	C
ATOM	1849	NH1	ARG	A	130	37.620	13.808	4.337	1.00	26.77	N
ATOM	1852	NH2	ARG	A	130	36.524	15.209	2.775	1.00	23.08	N
ATOM	1855	C	ARG	A	130	39.990	18.543	5.958	1.00	19.20	C
ATOM	1856	O	ARG	A	130	40.816	19.255	5.352	1.00	20.50	O
ATOM	1857	N	THR	A	131	38.740	18.915	6.155	1.00	18.72	N
ATOM	1859	CA	THR	A	131	38.127	20.089	5.461	1.00	19.43	C
ATOM	1861	CB	THR	A	131	36.673	19.866	5.244	1.00	20.43	C
ATOM	1863	OG1	THR	A	131	35.973	19.754	6.517	1.00	18.62	O
ATOM	1865	CG2	THR	A	131	36.421	18.548	4.449	1.00	22.94	C
ATOM	1869	C	THR	A	131	38.262	21.415	6.203	1.00	20.40	C
ATOM	1870	O	THR	A	131	37.906	22.461	5.657	1.00	20.95	O
ATOM	1871	N	GLY	A	132	38.758	21.356	7.431	1.00	18.57	N
ATOM	1873	CA	GLY	A	132	38.841	22.513	8.289	1.00	19.51	C
ATOM	1876	C	GLY	A	132	37.464	23.129	8.581	1.00	20.63	C
ATOM	1877	O	GLY	A	132	37.313	24.336	8.829	1.00	23.12	O
ATOM	1878	N	SER	A	133	36.442	22.287	8.646	1.00	18.55	N
ATOM	1880	CA	SER	A	133	35.094	22.754	8.904	1.00	18.11	C
ATOM	1882	CB	SER	A	133	34.080	21.819	8.260	1.00	18.42	C
ATOM	1885	OG	SER	A	133	34.242	21.666	6.844	1.00	21.03	O
ATOM	1887	C	SER	A	133	34.768	22.836	10.427	1.00	16.26	C
ATOM	1888	O	SER	A	133	35.348	22.145	11.284	1.00	15.54	O
ATOM	1889	N	LYS	A	134	33.798	23.687	10.720	1.00	16.27	N
ATOM	1891	CA	LYS	A	134	33.275	23.830	12.096	1.00	15.54	C
ATOM	1893	CB	LYS	A	134	32.921	25.274	12.419	1.00	15.50	C
ATOM	1896	CG	LYS	A	134	34.154	26.176	12.525	1.00	18.18	C
ATOM	1899	CD	LYS	A	134	33.819	27.647	12.502	1.00	25.94	C
ATOM	1902	CE	LYS	A	134	35.064	28.567	12.191	1.00	30.57	C
ATOM	1905	NZ	LYS	A	134	36.391	28.051	12.564	1.00	34.14	N
ATOM	1909	C	LYS	A	134	32.032	22.951	12.094	1.00	13.21	C
ATOM	1910	O	LYS	A	134	31.121	23.177	11.349	1.00	14.18	O
ATOM	1911	N	VAL	A	135	32.015	21.919	12.921	1.00	12.06	N
ATOM	1913	CA	VAL	A	135	30.964	20.957	12.863	1.00	12.02	C
ATOM	1915	CB	VAL	A	135	31.487	19.632	12.321	1.00	13.28	C
ATOM	1917	CG1	VAL	A	135	30.363	18.596	12.114	1.00	14.27	C
ATOM	1921	CG2	VAL	A	135	32.322	19.867	11.006	1.00	14.42	C
ATOM	1925	C	VAL	A	135	30.383	20.673	14.241	1.00	11.74	C
ATOM	1926	O	VAL	A	135	31.097	20.566	15.220	1.00	11.76	O
ATOM	1927	N	VAL	A	136	29.071	20.604	14.286	1.00	11.28	N
ATOM	1929	CA	VAL	A	136	28.389	20.206	15.478	1.00	10.73	C
ATOM	1931	CB	VAL	A	136	27.285	21.177	15.819	1.00	11.25	C
ATOM	1933	CG1	VAL	A	136	26.576	20.755	17.127	1.00	13.78	C
ATOM	1937	CG2	VAL	A	136	27.897	22.594	16.013	1.00	12.65	C
ATOM	1941	C	VAL	A	136	27.702	18.852	15.159	1.00	11.22	C
ATOM	1942	O	VAL	A	136	26.973	18.747	14.178	1.00	11.53	O
ATOM	1943	N	ILE	A	137	27.928	17.850	15.993	1.00	9.65	N
ATOM	1945	CA	ILE	A	137	27.255	16.573	15.854	1.00	10.61	C
ATOM	1947	CB	ILE	A	137	28.113	15.459	16.381	1.00	9.23	C
ATOM	1949	CG1	ILE	A	137	29.215	15.121	15.395	1.00	11.83	C
ATOM	1952	CD1	ILE	A	137	30.266	14.104	15.930	1.00	11.56	C
ATOM	1956	CG2	ILE	A	137	27.238	14.230	16.611	1.00	10.38	C
ATOM	1960	C	ILE	A	137	25.993	16.610	16.690	1.00	10.44	C

ATOM	1961	O	ILE	A	137	26.031	17.014	17.869	1.00	11.92	O
ATOM	1962	N	ASN	A	138	24.899	16.203	16.096	1.00	9.00	N
ATOM	1964	CA	ASN	A	138	23.654	15.942	16.764	1.00	10.52	C
ATOM	1966	CB	ASN	A	138	22.494	16.601	15.996	1.00	8.55	C
ATOM	1969	CG	ASN	A	138	21.146	16.503	16.715	1.00	12.38	C
ATOM	1970	OD1	ASN	A	138	20.648	17.515	17.236	1.00	10.74	O
ATOM	1971	ND2	ASN	A	138	20.519	15.297	16.722	1.00	9.55	N
ATOM	1974	C	ASN	A	138	23.376	14.477	16.861	1.00	10.74	C
ATOM	1975	O	ASN	A	138	23.256	13.799	15.833	1.00	9.80	O
ATOM	1976	N	MET	A	139	23.208	13.987	18.091	1.00	9.89	N
ATOM	1978	CA	MET	A	139	22.830	12.585	18.304	1.00	10.28	C
ATOM	1980	CB	MET	A	139	23.975	11.764	18.906	1.00	9.62	C
ATOM	1983	CG	MET	A	139	24.984	11.345	17.895	1.00	8.67	C
ATOM	1986	SD	MET	A	139	26.240	10.206	18.525	1.00	11.34	S
ATOM	1987	CE	MET	A	139	27.161	11.324	19.556	1.00	13.56	C
ATOM	1991	C	MET	A	139	21.581	12.474	19.162	1.00	10.20	C
ATOM	1992	O	MET	A	139	21.587	12.497	20.413	1.00	9.22	O
ATOM	1993	N	SER	A	140	20.467	12.424	18.458	1.00	10.57	N
ATOM	1995	CA	SER	A	140	19.166	12.207	19.083	1.00	10.10	C
ATOM	1997	CB	SER	A	140	18.082	12.817	18.201	1.00	10.22	C
ATOM	2000	OG	SER	A	140	18.142	14.229	18.264	1.00	11.42	O
ATOM	2002	C	SER	A	140	18.959	10.705	19.255	1.00	11.04	C
ATOM	2003	O	SER	A	140	18.006	10.119	18.716	1.00	10.43	O
ATOM	2004	N	LEU	A	141	19.844	10.063	20.011	1.00	10.62	N
ATOM	2006	CA	LEU	A	141	19.890	8.627	20.116	1.00	10.50	C
ATOM	2008	CB	LEU	A	141	20.446	8.014	18.833	1.00	10.74	C
ATOM	2011	CG	LEU	A	141	21.881	8.483	18.439	1.00	11.49	C
ATOM	2013	CD1	LEU	A	141	22.939	7.897	19.316	1.00	11.20	C
ATOM	2017	CD2	LEU	A	141	22.119	8.057	17.001	1.00	12.54	C
ATOM	2021	C	LEU	A	141	20.748	8.223	21.297	1.00	9.69	C
ATOM	2022	O	LEU	A	141	21.402	9.060	21.892	1.00	9.38	O
ATOM	2023	N	GLY	A	142	20.640	6.975	21.689	1.00	11.48	N
ATOM	2025	CA	GLY	A	142	21.450	6.472	22.789	1.00	10.69	C
ATOM	2028	C	GLY	A	142	21.046	5.146	23.335	1.00	9.74	C
ATOM	2029	O	GLY	A	142	20.283	4.413	22.660	1.00	12.20	O
ATOM	2030	N	SER	A	143	21.517	4.850	24.562	1.00	11.68	N
ATOM	2032	CA	SER	A	143	21.200	3.610	25.308	1.00	11.10	C
ATOM	2034	CB	SER	A	143	22.187	2.489	25.050	1.00	11.52	C
ATOM	2037	OG	SER	A	143	23.517	2.918	25.316	1.00	11.14	O
ATOM	2039	C	SER	A	143	21.272	3.995	26.777	1.00	12.09	C
ATOM	2040	O	SER	A	143	21.941	4.966	27.161	1.00	11.62	O
ATOM	2041	N	SER	A	144	20.523	3.292	27.587	1.00	11.90	N
ATOM	2043	CA	SER	A	144	20.527	3.552	28.992	1.00	11.92	C
ATOM	2045	CB	SER	A	144	19.513	2.623	29.653	1.00	13.61	C
ATOM	2048	OG	SER	A	144	19.521	2.848	31.017	1.00	18.36	O
ATOM	2050	C	SER	A	144	21.903	3.362	29.593	1.00	13.78	C
ATOM	2051	O	SER	A	144	22.341	4.161	30.401	1.00	14.05	O
ATOM	2052	N	ALA	A	145	22.551	2.278	29.189	1.00	12.68	N
ATOM	2054	CA	ALA	A	145	23.892	1.972	29.678	1.00	11.54	C
ATOM	2056	CB	ALA	A	145	24.135	0.503	29.488	1.00	12.43	C
ATOM	2060	C	ALA	A	145	24.956	2.745	28.886	1.00	12.26	C
ATOM	2061	O	ALA	A	145	24.814	3.001	27.712	1.00	12.18	O
ATOM	2062	N	LYS	A	146	26.067	3.066	29.521	1.00	10.71	N
ATOM	2064	CA	LYS	A	146	27.184	3.640	28.760	1.00	11.08	C
ATOM	2066	CB	LYS	A	146	28.219	4.095	29.754	1.00	10.62	C
ATOM	2069	CG	LYS	A	146	29.563	4.535	29.197	1.00	13.37	C
ATOM	2072	CD	LYS	A	146	30.506	5.206	30.245	1.00	14.55	C
ATOM	2075	CE	LYS	A	146	31.796	5.638	29.643	1.00	17.59	C

ATOM	2078	NZ	LYS	A	146	32.732	6.238	30.665	1.00	17.20	N
ATOM	2082	C	LYS	A	146	27.767	2.559	27.834	1.00	8.93	C
ATOM	2083	O	LYS	A	146	27.978	1.383	28.241	1.00	11.42	O
ATOM	2084	N	ASP	A	147	28.075	2.956	26.621	1.00	10.15	N
ATOM	2086	CA	ASP	A	147	28.694	2.129	25.575	1.00	10.08	C
ATOM	2088	CB	ASP	A	147	27.843	2.189	24.296	1.00	10.84	C
ATOM	2091	CG	ASP	A	147	28.460	1.509	23.117	1.00	11.61	C
ATOM	2092	OD1	ASP	A	147	29.701	1.630	22.895	1.00	11.69	O
ATOM	2093	OD2	ASP	A	147	27.753	0.879	22.305	1.00	10.96	O
ATOM	2094	C	ASP	A	147	30.057	2.784	25.353	1.00	10.79	C
ATOM	2095	O	ASP	A	147	30.163	3.902	24.859	1.00	9.34	O
ATOM	2096	N	SER	A	148	31.104	2.055	25.717	1.00	9.95	N
ATOM	2098	CA	SER	A	148	32.450	2.588	25.641	1.00	11.43	C
ATOM	2100	CB	SER	A	148	33.431	1.838	26.533	1.00	11.86	C
ATOM	2103	OG	SER	A	148	33.164	2.051	27.904	1.00	13.07	O
ATOM	2105	C	SER	A	148	32.999	2.765	24.221	1.00	12.17	C
ATOM	2106	O	SER	A	148	33.958	3.537	24.021	1.00	10.72	O
ATOM	2107	N	LEU	A	149	32.471	1.997	23.269	1.00	9.59	N
ATOM	2109	CA	LEU	A	149	32.936	2.120	21.909	1.00	10.95	C
ATOM	2111	CB	LEU	A	149	32.374	1.029	21.030	1.00	11.13	C
ATOM	2114	CG	LEU	A	149	32.863	1.087	19.569	1.00	13.82	C
ATOM	2116	CD1	LEU	A	149	34.404	0.961	19.536	1.00	14.72	C
ATOM	2120	CD2	LEU	A	149	32.162	0.036	18.699	1.00	15.05	C
ATOM	2124	C	LEU	A	149	32.474	3.511	21.419	1.00	10.85	C
ATOM	2125	O	LEU	A	149	33.201	4.268	20.807	1.00	10.58	O
ATOM	2126	N	ILE	A	150	31.223	3.823	21.649	1.00	9.24	N
ATOM	2128	CA	ILE	A	150	30.671	5.127	21.255	1.00	9.06	C
ATOM	2130	CB	ILE	A	150	29.145	5.136	21.471	1.00	8.95	C
ATOM	2132	CG1	ILE	A	150	28.499	4.376	20.337	1.00	9.94	C
ATOM	2135	CD1	ILE	A	150	27.038	4.154	20.508	1.00	11.53	C
ATOM	2139	CG2	ILE	A	150	28.601	6.553	21.538	1.00	11.45	C
ATOM	2143	C	ILE	A	150	31.433	6.226	22.052	1.00	7.79	C
ATOM	2144	O	ILE	A	150	31.793	7.297	21.500	1.00	8.15	O
ATOM	2145	N	ALA	A	151	31.724	5.956	23.300	1.00	8.34	N
ATOM	2147	CA	ALA	A	151	32.396	6.930	24.152	1.00	9.35	C
ATOM	2149	CB	ALA	A	151	32.479	6.402	25.577	1.00	10.22	C
ATOM	2153	C	ALA	A	151	33.796	7.240	23.629	1.00	9.49	C
ATOM	2154	O	ALA	A	151	34.215	8.422	23.583	1.00	9.45	O
ATOM	2155	N	SER	A	152	34.508	6.177	23.181	1.00	10.40	N
ATOM	2157	CA	SER	A	152	35.823	6.371	22.613	1.00	11.13	C
ATOM	2159	CB	SER	A	152	36.466	5.047	22.278	1.00	10.46	C
ATOM	2162	OG	SER	A	152	37.628	5.216	21.460	1.00	13.86	O
ATOM	2164	C	SER	A	152	35.737	7.285	21.349	1.00	11.17	C
ATOM	2165	O	SER	A	152	36.585	8.207	21.144	1.00	11.47	O
ATOM	2166	N	ALA	A	153	34.688	7.103	20.578	1.00	11.26	N
ATOM	2168	CA	ALA	A	153	34.476	7.917	19.358	1.00	11.23	C
ATOM	2170	CB	ALA	A	153	33.413	7.295	18.527	1.00	12.05	C
ATOM	2174	C	ALA	A	153	34.143	9.349	19.699	1.00	11.53	C
ATOM	2175	O	ALA	A	153	34.699	10.314	19.103	1.00	11.12	O
ATOM	2176	N	VAL	A	154	33.285	9.529	20.695	1.00	9.67	N
ATOM	2178	CA	VAL	A	154	32.941	10.878	21.104	1.00	9.77	C
ATOM	2180	CB	VAL	A	154	31.908	10.810	22.223	1.00	10.26	C
ATOM	2182	CG1	VAL	A	154	31.833	12.136	22.988	1.00	12.19	C
ATOM	2186	CG2	VAL	A	154	30.583	10.402	21.661	1.00	11.04	C
ATOM	2190	C	VAL	A	154	34.229	11.606	21.565	1.00	11.02	C
ATOM	2191	O	VAL	A	154	34.449	12.779	21.212	1.00	11.61	O
ATOM	2192	N	ASP	A	155	35.069	10.954	22.367	1.00	10.47	N
ATOM	2194	CA	ASP	A	155	36.309	11.603	22.838	1.00	12.38	C

ATOM	2196	CB	ASP	A	155	37.040	10.744	23.859	1.00	13.32	C
ATOM	2199	CG	ASP	A	155	36.328	10.668	25.183	1.00	19.66	C
ATOM	2200	OD1	ASP	A	155	35.449	11.508	25.455	1.00	21.98	O
ATOM	2201	OD2	ASP	A	155	36.604	9.813	26.030	1.00	21.73	O
ATOM	2202	C	ASP	A	155	37.242	11.932	21.674	1.00	13.46	C
ATOM	2203	O	ASP	A	155	37.928	12.926	21.695	1.00	12.65	O
ATOM	2204	N	TYR	A	156	37.308	11.034	20.694	1.00	12.30	N
ATOM	2206	CA	TYR	A	156	38.119	11.263	19.510	1.00	11.91	C
ATOM	2208	CB	TYR	A	156	37.992	10.073	18.607	1.00	12.85	C
ATOM	2211	CG	TYR	A	156	38.753	10.140	17.309	1.00	13.57	C
ATOM	2212	CD1	TYR	A	156	40.154	9.965	17.286	1.00	16.30	C
ATOM	2214	CE1	TYR	A	156	40.822	9.989	16.093	1.00	15.71	C
ATOM	2216	CZ	TYR	A	156	40.136	10.172	14.899	1.00	20.85	C
ATOM	2217	OH	TYR	A	156	40.795	10.142	13.677	1.00	19.47	O
ATOM	2219	CE2	TYR	A	156	38.771	10.352	14.883	1.00	14.75	C
ATOM	2221	CD2	TYR	A	156	38.096	10.349	16.111	1.00	14.20	C
ATOM	2223	C	TYR	A	156	37.653	12.497	18.764	1.00	11.70	C
ATOM	2224	O	TYR	A	156	38.463	13.343	18.408	1.00	12.40	O
ATOM	2225	N	ALA	A	157	36.332	12.649	18.630	1.00	11.59	N
ATOM	2227	CA	ALA	A	157	35.773	13.776	17.895	1.00	10.92	C
ATOM	2229	CB	ALA	A	157	34.319	13.493	17.547	1.00	11.98	C
ATOM	2233	C	ALA	A	157	35.926	15.058	18.670	1.00	11.69	C
ATOM	2234	O	ALA	A	157	36.214	16.117	18.072	1.00	11.27	O
ATOM	2235	N	TYR	A	158	35.740	14.996	19.983	1.00	11.31	N
ATOM	2237	CA	TYR	A	158	35.855	16.210	20.809	1.00	12.56	C
ATOM	2239	CB	TYR	A	158	35.410	15.940	22.243	1.00	12.28	C
ATOM	2242	CG	TYR	A	158	35.147	17.188	23.090	1.00	9.96	C
ATOM	2243	CD1	TYR	A	158	34.015	17.937	22.878	1.00	11.56	C
ATOM	2245	CE1	TYR	A	158	33.754	19.051	23.629	1.00	13.20	C
ATOM	2247	CZ	TYR	A	158	34.635	19.477	24.580	1.00	13.62	C
ATOM	2248	OH	TYR	A	158	34.370	20.612	25.295	1.00	12.22	O
ATOM	2250	CE2	TYR	A	158	35.813	18.809	24.787	1.00	13.48	C
ATOM	2252	CD2	TYR	A	158	36.078	17.647	24.028	1.00	12.56	C
ATOM	2254	C	TYR	A	158	37.308	16.655	20.783	1.00	12.48	C
ATOM	2255	O	TYR	A	158	37.591	17.853	20.822	1.00	12.68	O
ATOM	2256	N	GLY	A	159	38.207	15.683	20.642	1.00	12.38	N
ATOM	2258	CA	GLY	A	159	39.628	15.978	20.651	1.00	13.17	C
ATOM	2261	C	GLY	A	159	40.055	16.611	19.371	1.00	13.46	C
ATOM	2262	O	GLY	A	159	41.161	17.165	19.297	1.00	14.28	O
ATOM	2263	N	LYS	A	160	39.238	16.495	18.350	1.00	12.48	N
ATOM	2265	CA	LYS	A	160	39.486	17.099	17.035	1.00	14.66	C
ATOM	2267	CB	LYS	A	160	39.324	16.046	15.953	1.00	15.36	C
ATOM	2270	CG	LYS	A	160	40.421	14.964	15.992	1.00	20.16	C
ATOM	2273	CD	LYS	A	160	40.057	13.848	15.058	1.00	25.00	C
ATOM	2276	CE	LYS	A	160	41.183	13.408	14.161	1.00	31.38	C
ATOM	2279	NZ	LYS	A	160	41.602	14.404	13.204	1.00	30.54	N
ATOM	2283	C	LYS	A	160	38.603	18.344	16.761	1.00	14.03	C
ATOM	2284	O	LYS	A	160	38.469	18.786	15.621	1.00	12.37	O
ATOM	2285	N	GLY	A	161	38.076	18.954	17.829	1.00	13.97	N
ATOM	2287	CA	GLY	A	161	37.363	20.230	17.751	1.00	13.11	C
ATOM	2290	C	GLY	A	161	35.928	20.180	17.281	1.00	12.99	C
ATOM	2291	O	GLY	A	161	35.434	21.185	16.743	1.00	14.25	O
ATOM	2292	N	VAL	A	162	35.269	19.020	17.395	1.00	11.44	N
ATOM	2294	CA	VAL	A	162	33.858	18.848	16.972	1.00	10.32	C
ATOM	2296	CB	VAL	A	162	33.621	17.492	16.309	1.00	11.03	C
ATOM	2298	CG1	VAL	A	162	32.146	17.268	15.950	1.00	11.59	C
ATOM	2302	CG2	VAL	A	162	34.438	17.378	15.034	1.00	13.60	C
ATOM	2306	C	VAL	A	162	32.991	18.918	18.219	1.00	10.43	C

ATOM	2307	O	VAL	A	162	33.306	18.259	19.222	1.00	11.54	O
ATOM	2308	N	LEU	A	163	31.965	19.748	18.217	1.00	9.11	N
ATOM	2310	CA	LEU	A	163	31.075	19.817	19.382	1.00	10.40	C
ATOM	2312	CB	LEU	A	163	30.278	21.105	19.344	1.00	11.53	C
ATOM	2315	CG	LEU	A	163	29.336	21.334	20.515	1.00	10.22	C
ATOM	2317	CD1	LEU	A	163	30.163	21.561	21.748	1.00	12.89	C
ATOM	2321	CD2	LEU	A	163	28.486	22.497	20.248	1.00	13.67	C
ATOM	2325	C	LEU	A	163	30.118	18.647	19.257	1.00	10.89	C
ATOM	2326	O	LEU	A	163	29.620	18.367	18.176	1.00	13.34	O
ATOM	2327	N	ILE	A	164	29.832	17.975	20.347	1.00	11.01	N
ATOM	2329	CA	ILE	A	164	28.860	16.890	20.383	1.00	9.92	C
ATOM	2331	CB	ILE	A	164	29.500	15.573	20.908	1.00	10.24	C
ATOM	2333	CG1	ILE	A	164	30.616	15.070	19.976	1.00	13.39	C
ATOM	2336	CD1	ILE	A	164	31.893	15.389	20.491	1.00	16.69	C
ATOM	2340	CG2	ILE	A	164	28.496	14.458	20.907	1.00	12.88	C
ATOM	2344	C	ILE	A	164	27.673	17.259	21.275	1.00	10.29	C
ATOM	2345	O	ILE	A	164	27.851	17.505	22.479	1.00	10.17	O
ATOM	2346	N	VAL	A	165	26.489	17.191	20.694	1.00	9.19	N
ATOM	2348	CA	VAL	A	165	25.257	17.479	21.391	1.00	9.03	C
ATOM	2350	CB	VAL	A	165	24.576	18.708	20.753	1.00	10.21	C
ATOM	2352	CG1	VAL	A	165	23.300	19.053	21.542	1.00	9.33	C
ATOM	2356	CG2	VAL	A	165	25.483	19.888	20.715	1.00	11.01	C
ATOM	2360	C	VAL	A	165	24.360	16.245	21.311	1.00	8.47	C
ATOM	2361	O	VAL	A	165	24.193	15.681	20.222	1.00	10.40	O
ATOM	2362	N	ALA	A	166	23.833	15.747	22.452	1.00	9.28	N
ATOM	2364	CA	ALA	A	166	23.163	14.469	22.484	1.00	8.57	C
ATOM	2366	CB	ALA	A	166	24.104	13.327	22.794	1.00	9.70	C
ATOM	2370	C	ALA	A	166	22.011	14.454	23.489	1.00	9.40	C
ATOM	2371	O	ALA	A	166	22.028	15.186	24.476	1.00	9.37	O
ATOM	2372	N	ALA	A	167	21.000	13.646	23.186	1.00	10.21	N
ATOM	2374	CA	ALA	A	167	19.794	13.637	23.965	1.00	10.10	C
ATOM	2376	CB	ALA	A	167	18.747	12.726	23.251	1.00	11.66	C
ATOM	2380	C	ALA	A	167	20.086	13.087	25.329	1.00	10.38	C
ATOM	2381	O	ALA	A	167	20.787	12.038	25.431	1.00	8.93	O
ATOM	2382	N	ALA	A	168	19.424	13.572	26.360	1.00	10.36	N
ATOM	2384	CA	ALA	A	168	19.623	13.036	27.685	1.00	10.56	C
ATOM	2386	CB	ALA	A	168	19.014	13.978	28.698	1.00	11.45	C
ATOM	2390	C	ALA	A	168	19.026	11.631	27.894	1.00	10.08	C
ATOM	2391	O	ALA	A	168	19.441	10.860	28.771	1.00	10.97	O
ATOM	2392	N	GLY	A	169	18.020	11.315	27.108	1.00	9.80	N
ATOM	2394	CA	GLY	A	169	17.216	10.125	27.318	1.00	9.88	C
ATOM	2397	C	GLY	A	169	15.777	10.485	27.780	1.00	11.11	C
ATOM	2398	O	GLY	A	169	15.483	11.623	28.208	1.00	10.34	O
ATOM	2399	N	ASN	A	170	14.882	9.492	27.676	1.00	11.54	N
ATOM	2401	CA	ASN	A	170	13.483	9.636	28.090	1.00	11.53	C
ATOM	2403	CB	ASN	A	170	12.579	9.382	26.872	1.00	11.78	C
ATOM	2406	CG	ASN	A	170	12.911	10.285	25.682	1.00	13.65	C
ATOM	2407	OD1	ASN	A	170	13.358	11.427	25.856	1.00	14.26	O
ATOM	2408	ND2	ASN	A	170	12.666	9.791	24.465	1.00	10.92	N
ATOM	2411	C	ASN	A	170	13.116	8.658	29.184	1.00	12.69	C
ATOM	2412	O	ASN	A	170	12.046	8.036	29.123	1.00	12.66	O
ATOM	2413	N	SER	A	171	13.989	8.483	30.170	1.00	12.61	N
ATOM	2415	CA	SER	A	171	13.754	7.487	31.223	1.00	13.48	C
ATOM	2417	CB	SER	A	171	15.025	6.692	31.423	1.00	14.78	C
ATOM	2420	OG	SER	A	171	15.277	5.967	30.233	1.00	13.11	O
ATOM	2422	C	SER	A	171	13.308	8.147	32.538	1.00	13.22	C
ATOM	2423	O	SER	A	171	13.429	7.526	33.583	1.00	14.40	O
ATOM	2424	N	GLY	A	172	12.811	9.371	32.496	1.00	14.32	N

ATOM	2426	CA	GLY	A	172	12.428	10.098	33.710	1.00	14.13	C
ATOM	2429	C	GLY	A	172	11.127	9.606	34.292	1.00	15.66	C
ATOM	2430	O	GLY	A	172	10.473	8.814	33.614	1.00	15.22	O
ATOM	2431	N	SER	A	173	10.681	10.134	35.424	1.00	14.94	N
ATOM	2433	CA	SER	A	173	11.269	11.278	36.134	1.00	16.57	C
ATOM	2435	CB	SER	A	173	10.144	12.174	36.639	1.00	17.91	C
ATOM	2438	OG	SER	A	173	9.384	11.435	37.607	1.00	18.04	O
ATOM	2440	C	SER	A	173	12.196	10.908	37.265	1.00	16.47	C
ATOM	2441	O	SER	A	173	12.751	11.790	37.970	1.00	15.55	O
ATOM	2442	N	GLY	A	174	12.476	9.615	37.359	1.00	15.06	N
ATOM	2444	CA	GLY	A	174	13.318	9.075	38.400	1.00	16.35	C
ATOM	2447	C	GLY	A	174	14.715	9.629	38.233	1.00	17.64	C
ATOM	2448	O	GLY	A	174	15.159	9.906	37.086	1.00	17.46	O
ATOM	2449	N	SER	A	175	15.404	9.827	39.351	1.00	17.08	N
ATOM	2451	CA	SER	A	175	16.752	10.404	39.336	1.00	18.22	C
ATOM	2453	CB	SER	A	175	17.129	10.794	40.759	1.00	19.80	C
ATOM	2456	OG	SER	A	175	16.121	11.654	41.308	1.00	21.20	O
ATOM	2458	C	SER	A	175	17.783	9.457	38.777	1.00	16.85	C
ATOM	2459	O	SER	A	175	17.638	8.238	38.884	1.00	15.37	O
ATOM	2460	N	ASN	A	176	18.838	10.010	38.168	1.00	16.57	N
ATOM	2462	CA	ASN	A	176	19.966	9.230	37.675	1.00	15.32	C
ATOM	2464	CB	ASN	A	176	20.679	8.475	38.817	1.00	17.33	C
ATOM	2467	CG	ASN	A	176	22.174	8.352	38.565	1.00	20.64	C
ATOM	2468	OD1	ASN	A	176	22.676	9.003	37.649	1.00	19.65	O
ATOM	2469	ND2	ASN	A	176	22.881	7.508	39.336	1.00	23.68	N
ATOM	2472	C	ASN	A	176	19.634	8.250	36.592	1.00	15.22	C
ATOM	2473	O	ASN	A	176	20.208	7.146	36.528	1.00	16.86	O
ATOM	2474	N	THR	A	177	18.718	8.639	35.723	1.00	14.53	N
ATOM	2476	CA	THR	A	177	18.299	7.815	34.612	1.00	14.30	C
ATOM	2478	CB	THR	A	177	16.768	7.831	34.488	1.00	13.61	C
ATOM	2480	OG1	THR	A	177	16.255	9.161	34.632	1.00	12.76	O
ATOM	2482	CG2	THR	A	177	16.053	7.001	35.629	1.00	14.89	C
ATOM	2486	C	THR	A	177	18.907	8.265	33.267	1.00	13.62	C
ATOM	2487	O	THR	A	177	18.555	7.704	32.213	1.00	14.34	O
ATOM	2488	N	ILE	A	178	19.736	9.305	33.324	1.00	12.33	N
ATOM	2490	CA	ILE	A	178	20.436	9.809	32.125	1.00	10.85	C
ATOM	2492	CB	ILE	A	178	21.473	10.886	32.543	1.00	11.28	C
ATOM	2494	CG1	ILE	A	178	22.118	11.576	31.337	1.00	11.95	C
ATOM	2497	CD1	ILE	A	178	22.981	12.833	31.722	1.00	12.82	C
ATOM	2501	CG2	ILE	A	178	22.550	10.300	33.406	1.00	11.10	C
ATOM	2505	C	ILE	A	178	21.057	8.663	31.350	1.00	10.78	C
ATOM	2506	O	ILE	A	178	21.582	7.715	31.950	1.00	10.96	O
ATOM	2507	N	GLY	A	179	20.973	8.706	30.032	1.00	9.07	N
ATOM	2509	CA	GLY	A	179	21.658	7.732	29.200	1.00	10.43	C
ATOM	2512	C	GLY	A	179	22.842	8.334	28.433	1.00	10.17	C
ATOM	2513	O	GLY	A	179	23.302	9.423	28.716	1.00	9.05	O
ATOM	2514	N	PHE	A	180	23.302	7.579	27.474	1.00	10.42	N
ATOM	2516	CA	PHE	A	180	24.566	7.766	26.771	1.00	9.90	C
ATOM	2518	CB	PHE	A	180	25.597	6.710	27.248	1.00	11.20	C
ATOM	2521	CG	PHE	A	180	25.926	6.868	28.691	1.00	10.40	C
ATOM	2522	CD1	PHE	A	180	25.089	6.304	29.673	1.00	12.43	C
ATOM	2524	CE1	PHE	A	180	25.346	6.539	31.013	1.00	13.80	C
ATOM	2526	CZ	PHE	A	180	26.377	7.353	31.379	1.00	14.77	C
ATOM	2528	CE2	PHE	A	180	27.195	7.936	30.428	1.00	14.15	C
ATOM	2530	CD2	PHE	A	180	26.951	7.710	29.086	1.00	12.50	C
ATOM	2532	C	PHE	A	180	24.307	7.663	25.268	1.00	10.49	C
ATOM	2533	O	PHE	A	180	23.545	6.804	24.833	1.00	11.55	O
ATOM	2534	N	PRO	A	181	25.023	8.448	24.458	1.00	9.50	N

ATOM	2535	CA	PRO	A	181	26.196	9.246	24.890	1.00	9.13	C
ATOM	2537	CB	PRO	A	181	26.937	9.496	23.524	1.00	9.24	C
ATOM	2540	CG	PRO	A	181	25.855	9.591	22.649	1.00	11.31	C
ATOM	2543	CD	PRO	A	181	24.874	8.496	23.002	1.00	10.03	C
ATOM	2546	C	PRO	A	181	25.983	10.570	25.610	1.00	10.79	C
ATOM	2547	O	PRO	A	181	26.959	11.251	25.986	1.00	9.76	O
ATOM	2548	N	GLY	A	182	24.743	11.019	25.752	1.00	10.07	N
ATOM	2550	CA	GLY	A	182	24.480	12.260	26.450	1.00	10.91	C
ATOM	2553	C	GLY	A	182	25.260	12.460	27.748	1.00	10.65	C
ATOM	2554	O	GLY	A	182	25.843	13.532	27.983	1.00	10.24	O
ATOM	2555	N	GLY	A	183	25.246	11.400	28.570	1.00	10.23	N
ATOM	2557	CA	GLY	A	183	25.860	11.370	29.888	1.00	11.34	C
ATOM	2560	C	GLY	A	183	27.370	11.393	29.929	1.00	11.75	C
ATOM	2561	O	GLY	A	183	27.957	11.394	31.025	1.00	10.33	O
ATOM	2562	N	LEU	A	184	28.007	11.351	28.761	1.00	11.62	N
ATOM	2564	CA	LEU	A	184	29.474	11.436	28.718	1.00	11.77	C
ATOM	2566	CB	LEU	A	184	30.022	11.038	27.369	1.00	10.76	C
ATOM	2569	CG	LEU	A	184	29.612	9.640	26.946	1.00	13.28	C
ATOM	2571	CD1	LEU	A	184	29.958	9.447	25.484	1.00	13.01	C
ATOM	2575	CD2	LEU	A	184	30.306	8.563	27.839	1.00	15.87	C
ATOM	2579	C	LEU	A	184	29.966	12.827	29.034	1.00	11.00	C
ATOM	2580	O	LEU	A	184	29.321	13.827	28.682	1.00	10.77	O
ATOM	2581	N	VAL	A	185	31.180	12.922	29.584	1.00	11.17	N
ATOM	2583	CA	VAL	A	185	31.673	14.225	29.979	1.00	10.77	C
ATOM	2585	CB	VAL	A	185	32.994	14.115	30.811	1.00	13.00	C
ATOM	2587	CG1	VAL	A	185	33.978	13.569	30.013	1.00	16.83	C
ATOM	2591	CG2	VAL	A	185	33.500	15.504	31.144	1.00	16.03	C
ATOM	2595	C	VAL	A	185	31.868	15.172	28.842	1.00	9.95	C
ATOM	2596	O	VAL	A	185	31.683	16.370	28.972	1.00	10.97	O
ATOM	2597	N	ASN	A	186	32.181	14.614	27.684	1.00	10.43	N
ATOM	2599	CA	ASN	A	186	32.483	15.376	26.517	1.00	11.79	C
ATOM	2601	CB	ASN	A	186	33.763	14.865	25.836	1.00	13.55	C
ATOM	2604	CG	ASN	A	186	35.029	15.152	26.660	1.00	14.82	C
ATOM	2605	OD1	ASN	A	186	35.093	16.110	27.370	1.00	19.19	O
ATOM	2606	ND2	ASN	A	186	36.021	14.326	26.517	1.00	21.64	N
ATOM	2609	C	ASN	A	186	31.305	15.525	25.536	1.00	11.85	C
ATOM	2610	O	ASN	A	186	31.485	15.915	24.384	1.00	11.39	O
ATOM	2611	N	ALA	A	187	30.108	15.138	25.977	1.00	10.51	N
ATOM	2613	CA	ALA	A	187	28.904	15.382	25.179	1.00	11.08	C
ATOM	2615	CB	ALA	A	187	28.189	14.150	24.848	1.00	11.19	C
ATOM	2619	C	ALA	A	187	27.984	16.317	25.975	1.00	10.66	C
ATOM	2620	O	ALA	A	187	27.878	16.147	27.186	1.00	11.05	O
ATOM	2621	N	VAL	A	188	27.318	17.248	25.288	1.00	9.26	N
ATOM	2623	CA	VAL	A	188	26.326	18.148	25.895	1.00	9.21	C
ATOM	2625	CB	VAL	A	188	26.120	19.418	25.046	1.00	9.41	C
ATOM	2627	CG1	VAL	A	188	25.035	20.249	25.661	1.00	7.57	C
ATOM	2631	CG2	VAL	A	188	27.448	20.164	24.893	1.00	10.01	C
ATOM	2635	C	VAL	A	188	24.996	17.346	25.984	1.00	9.78	C
ATOM	2636	O	VAL	A	188	24.349	17.137	24.959	1.00	10.45	O
ATOM	2637	N	ALA	A	189	24.572	16.989	27.200	1.00	8.67	N
ATOM	2639	CA	ALA	A	189	23.325	16.236	27.430	1.00	9.35	C
ATOM	2641	CB	ALA	A	189	23.379	15.510	28.763	1.00	10.27	C
ATOM	2645	C	ALA	A	189	22.197	17.214	27.451	1.00	8.43	C
ATOM	2646	O	ALA	A	189	22.179	18.183	28.238	1.00	9.35	O
ATOM	2647	N	VAL	A	190	21.182	16.948	26.651	1.00	9.14	N
ATOM	2649	CA	VAL	A	190	20.084	17.882	26.554	1.00	8.32	C
ATOM	2651	CB	VAL	A	190	19.843	18.296	25.119	1.00	8.58	C
ATOM	2653	CG1	VAL	A	190	18.731	19.309	25.052	1.00	11.50	C

ATOM	2657	CG2	VAL	A	190	21.084	18.873	24.482	1.00	9.20	C
ATOM	2661	C	VAL	A	190	18.791	17.317	27.087	1.00	9.51	C
ATOM	2662	O	VAL	A	190	18.340	16.256	26.625	1.00	9.51	O
ATOM	2663	N	ALA	A	191	18.236	17.973	28.093	1.00	9.50	N
ATOM	2665	CA	ALA	A	191	16.934	17.559	28.685	1.00	10.18	C
ATOM	2667	CB	ALA	A	191	16.868	18.057	30.134	1.00	8.69	C
ATOM	2671	C	ALA	A	191	15.800	18.184	27.900	1.00	10.24	C
ATOM	2672	O	ALA	A	191	16.007	19.182	27.249	1.00	10.28	O
ATOM	2673	N	ALA	A	192	14.570	17.659	28.021	1.00	11.22	N
ATOM	2675	CA	ALA	A	192	13.428	18.171	27.272	1.00	11.79	C
ATOM	2677	CB	ALA	A	192	12.593	17.012	26.728	1.00	13.73	C
ATOM	2681	C	ALA	A	192	12.499	19.027	28.134	1.00	11.54	C
ATOM	2682	O	ALA	A	192	12.048	18.549	29.179	1.00	11.30	O
ATOM	2683	N	LEU	A	193	12.222	20.238	27.673	1.00	11.58	N
ATOM	2685	CA	LEU	A	193	11.194	21.103	28.258	1.00	11.55	C
ATOM	2687	CB	LEU	A	193	11.519	22.561	28.037	1.00	12.06	C
ATOM	2690	CG	LEU	A	193	12.844	23.095	28.613	1.00	10.40	C
ATOM	2692	CD1	LEU	A	193	13.137	24.484	28.211	1.00	9.32	C
ATOM	2696	CD2	LEU	A	193	12.752	22.903	30.081	1.00	13.29	C
ATOM	2700	C	LEU	A	193	9.852	20.802	27.577	1.00	14.05	C
ATOM	2701	O	LEU	A	193	9.814	20.460	26.414	1.00	13.73	O
ATOM	2702	N	GLU	A	194	8.755	21.004	28.305	1.00	13.56	N
ATOM	2704	CA	GLU	A	194	7.422	21.049	27.647	1.00	13.63	C
ATOM	2706	CB	GLU	A	194	6.472	20.125	28.359	1.00	12.74	C
ATOM	2709	CG	GLU	A	194	6.320	20.410	29.837	1.00	16.62	C
ATOM	2712	CD	GLU	A	194	5.490	19.404	30.603	1.00	19.10	C
ATOM	2713	OE1	GLU	A	194	5.288	18.280	30.118	1.00	20.53	O
ATOM	2714	OE2	GLU	A	194	5.153	19.744	31.765	1.00	17.20	O
ATOM	2715	C	GLU	A	194	6.934	22.460	27.699	1.00	14.48	C
ATOM	2716	O	GLU	A	194	7.502	23.275	28.431	1.00	13.32	O
ATOM	2717	N	ASN	A	195	5.862	22.778	26.954	1.00	14.74	N
ATOM	2719	CA	ASN	A	195	5.416	24.169	26.857	1.00	15.00	C
ATOM	2721	CB	ASN	A	195	4.773	24.467	25.479	1.00	16.14	C
ATOM	2724	CG	ASN	A	195	4.612	25.970	25.198	1.00	16.46	C
ATOM	2725	OD1	ASN	A	195	5.236	26.803	25.855	1.00	14.84	O
ATOM	2726	ND2	ASN	A	195	3.775	26.318	24.208	1.00	13.91	N
ATOM	2729	C	ASN	A	195	4.439	24.440	27.945	1.00	16.03	C
ATOM	2730	O	ASN	A	195	3.256	24.692	27.662	1.00	15.98	O
ATOM	2731	N	VAL	A	196	4.904	24.381	29.170	1.00	16.13	N
ATOM	2733	CA	VAL	A	196	4.106	24.623	30.344	1.00	16.89	C
ATOM	2735	CB	VAL	A	196	3.739	23.348	31.019	1.00	18.38	C
ATOM	2737	CG1	VAL	A	196	3.058	23.613	32.326	1.00	20.19	C
ATOM	2741	CG2	VAL	A	196	2.922	22.415	30.070	1.00	18.32	C
ATOM	2745	C	VAL	A	196	4.991	25.380	31.307	1.00	17.79	C
ATOM	2746	O	VAL	A	196	6.215	25.147	31.344	1.00	17.15	O
ATOM	2747	N	GLN	A	197	4.410	26.305	32.055	1.00	17.34	N
ATOM	2749	CA	GLN	A	197	5.171	27.048	33.060	1.00	16.33	C
ATOM	2751	CB	GLN	A	197	4.838	28.518	33.012	1.00	16.74	C
ATOM	2754	CG	GLN	A	197	4.987	29.169	31.720	1.00	16.89	C
ATOM	2757	CD	GLN	A	197	6.455	29.357	31.343	1.00	18.48	C
ATOM	2758	OE1	GLN	A	197	7.216	30.009	32.096	1.00	14.66	O
ATOM	2759	NE2	GLN	A	197	6.850	28.769	30.223	1.00	15.37	N
ATOM	2762	C	GLN	A	197	4.907	26.538	34.467	1.00	17.79	C
ATOM	2763	O	GLN	A	197	3.778	26.114	34.825	1.00	18.50	O
ATOM	2764	N	GLN	A	198	5.977	26.409	35.232	1.00	17.07	N
ATOM	2766	CA	GLN	A	198	5.879	25.977	36.627	1.00	17.39	C
ATOM	2768	CB	GLN	A	198	5.865	24.485	36.778	1.00	17.84	C
ATOM	2771	CG	GLN	A	198	5.744	24.058	38.164	1.00	18.38	C

ATOM	2774	CD	GLN	A	198	5.797	22.558	38.413	1.00	25.24	C
ATOM	2775	OE1	GLN	A	198	6.612	21.813	37.815	1.00	26.03	O
ATOM	2776	NE2	GLN	A	198	4.927	22.090	39.323	1.00	29.00	N
ATOM	2779	C	GLN	A	198	6.998	26.623	37.362	1.00	17.51	C
ATOM	2780	O	GLN	A	198	8.156	26.681	36.904	1.00	16.23	O
ATOM	2781	N	ASN	A	199	6.655	27.147	38.520	1.00	18.31	N
ATOM	2783	CA	ASN	A	199	7.612	27.890	39.321	1.00	19.42	C
ATOM	2785	CB	ASN	A	199	8.676	26.953	39.915	1.00	19.53	C
ATOM	2788	CG	ASN	A	199	8.107	25.949	40.861	1.00	24.01	C
ATOM	2789	OD1	ASN	A	199	7.226	26.254	41.691	1.00	23.71	O
ATOM	2790	ND2	ASN	A	199	8.598	24.738	40.769	1.00	25.09	N
ATOM	2793	C	ASN	A	199	8.285	29.018	38.592	1.00	20.51	C
ATOM	2794	O	ASN	A	199	9.491	29.356	38.863	1.00	20.07	O
ATOM	2795	N	GLY	A	200	7.533	29.653	37.712	1.00	19.65	N
ATOM	2797	CA	GLY	A	200	8.005	30.820	36.991	1.00	20.16	C
ATOM	2800	C	GLY	A	200	8.883	30.609	35.774	1.00	19.26	C
ATOM	2801	O	GLY	A	200	9.347	31.577	35.177	1.00	18.58	O
ATOM	2802	N	THR	A	201	9.091	29.348	35.384	1.00	17.29	N
ATOM	2804	CA	THR	A	201	9.876	29.045	34.196	1.00	16.82	C
ATOM	2806	CB	THR	A	201	11.327	28.563	34.596	1.00	16.41	C
ATOM	2808	OG1	THR	A	201	11.309	27.246	35.174	1.00	17.63	O
ATOM	2810	CG2	THR	A	201	11.954	29.437	35.622	1.00	17.27	C
ATOM	2814	C	THR	A	201	9.248	27.935	33.389	1.00	15.50	C
ATOM	2815	O	THR	A	201	8.267	27.356	33.817	1.00	14.83	O
ATOM	2816	N	TYR	A	202	9.845	27.608	32.230	1.00	15.66	N
ATOM	2818	CA	TYR	A	202	9.469	26.407	31.571	1.00	14.51	C
ATOM	2820	CB	TYR	A	202	10.308	26.183	30.300	1.00	15.38	C
ATOM	2823	CG	TYR	A	202	9.853	27.053	29.177	1.00	12.00	C
ATOM	2824	CD1	TYR	A	202	8.775	26.682	28.359	1.00	12.96	C
ATOM	2826	CE1	TYR	A	202	8.344	27.510	27.364	1.00	13.55	C
ATOM	2828	CZ	TYR	A	202	8.995	28.682	27.157	1.00	12.70	C
ATOM	2829	OH	TYR	A	202	8.586	29.559	26.172	1.00	14.68	O
ATOM	2831	CE2	TYR	A	202	10.027	29.063	27.961	1.00	14.77	C
ATOM	2833	CD2	TYR	A	202	10.441	28.245	28.957	1.00	13.26	C
ATOM	2835	C	TYR	A	202	9.637	25.229	32.488	1.00	14.45	C
ATOM	2836	O	TYR	A	202	10.442	25.231	33.415	1.00	14.03	O
ATOM	2837	N	ARG	A	203	8.894	24.168	32.206	1.00	14.53	N
ATOM	2839	CA	ARG	A	203	8.939	22.971	32.988	1.00	13.25	C
ATOM	2841	CB	ARG	A	203	7.454	22.543	33.262	1.00	14.52	C
ATOM	2844	CG	ARG	A	203	7.315	21.347	34.102	1.00	14.19	C
ATOM	2847	CD	ARG	A	203	5.795	21.083	34.523	1.00	15.99	C
ATOM	2850	NE	ARG	A	203	5.730	20.106	35.572	1.00	17.45	N
ATOM	2852	CZ	ARG	A	203	5.729	18.806	35.402	1.00	17.33	C
ATOM	2853	NH1	ARG	A	203	5.762	18.306	34.191	1.00	15.77	N
ATOM	2856	NH2	ARG	A	203	5.741	17.996	36.447	1.00	18.53	N
ATOM	2859	C	ARG	A	203	9.595	21.805	32.251	1.00	12.75	C
ATOM	2860	O	ARG	A	203	9.285	21.570	31.076	1.00	12.82	O
ATOM	2861	N	VAL	A	204	10.505	21.090	32.907	1.00	12.18	N
ATOM	2863	CA	VAL	A	204	11.043	19.877	32.378	1.00	11.32	C
ATOM	2865	CB	VAL	A	204	12.141	19.338	33.296	1.00	11.73	C
ATOM	2867	CG1	VAL	A	204	12.765	18.035	32.735	1.00	11.27	C
ATOM	2871	CG2	VAL	A	204	13.229	20.373	33.437	1.00	12.71	C
ATOM	2875	C	VAL	A	204	9.925	18.831	32.221	1.00	12.28	C
ATOM	2876	O	VAL	A	204	9.172	18.549	33.185	1.00	12.08	O
ATOM	2877	N	ALA	A	205	9.855	18.166	31.063	1.00	12.11	N
ATOM	2879	CA	ALA	A	205	8.882	17.061	30.935	1.00	12.63	C
ATOM	2881	CB	ALA	A	205	8.725	16.612	29.473	1.00	14.20	C
ATOM	2885	C	ALA	A	205	9.205	15.894	31.835	1.00	14.44	C

ATOM	2886	O	ALA	A	205	10.338	15.546	32.067	1.00	12.72	O
ATOM	2887	N	ASP	A	206	8.160	15.251	32.353	1.00	12.46	N
ATOM	2889	CA	ASP	A	206	8.351	14.138	33.226	1.00	14.42	C
ATOM	2891	CB	ASP	A	206	7.015	13.579	33.660	1.00	15.15	C
ATOM	2894	CG	ASP	A	206	6.273	14.456	34.620	1.00	20.28	C
ATOM	2895	OD1	ASP	A	206	6.717	15.552	35.015	1.00	16.78	O
ATOM	2896	OD2	ASP	A	206	5.164	14.025	35.032	1.00	21.17	O
ATOM	2897	C	ASP	A	206	9.161	13.020	32.556	1.00	13.89	C
ATOM	2898	O	ASP	A	206	9.920	12.348	33.229	1.00	15.04	O
ATOM	2899	N	PHE	A	207	9.016	12.821	31.246	1.00	11.78	N
ATOM	2901	CA	PHE	A	207	9.710	11.721	30.612	1.00	13.96	C
ATOM	2903	CB	PHE	A	207	9.163	11.360	29.213	1.00	13.87	C
ATOM	2906	CG	PHE	A	207	9.290	12.439	28.191	1.00	14.05	C
ATOM	2907	CD1	PHE	A	207	10.521	12.704	27.630	1.00	13.46	C
ATOM	2909	CE1	PHE	A	207	10.677	13.677	26.709	1.00	14.99	C
ATOM	2911	CZ	PHE	A	207	9.577	14.463	26.305	1.00	12.88	C
ATOM	2913	CE2	PHE	A	207	8.325	14.173	26.841	1.00	15.57	C
ATOM	2915	CD2	PHE	A	207	8.199	13.191	27.787	1.00	14.48	C
ATOM	2917	C	PHE	A	207	11.220	11.917	30.546	1.00	12.81	C
ATOM	2918	O	PHE	A	207	11.950	10.945	30.339	1.00	12.43	O
ATOM	2919	N	SER	A	208	11.670	13.163	30.626	1.00	13.24	N
ATOM	2921	CA	SER	A	208	13.099	13.459	30.389	1.00	12.69	C
ATOM	2923	CB	SER	A	208	13.277	14.980	30.333	1.00	13.69	C
ATOM	2926	OG	SER	A	208	14.593	15.399	30.016	1.00	11.00	O
ATOM	2928	C	SER	A	208	13.997	12.799	31.432	1.00	11.85	C
ATOM	2929	O	SER	A	208	13.726	12.841	32.612	1.00	12.56	O
ATOM	2930	N	SER	A	209	15.095	12.168	31.001	1.00	11.34	N
ATOM	2932	CA	SER	A	209	15.961	11.503	31.941	1.00	12.26	C
ATOM	2934	CB	SER	A	209	17.003	10.655	31.240	1.00	10.68	C
ATOM	2937	OG	SER	A	209	16.442	9.566	30.515	1.00	11.25	O
ATOM	2939	C	SER	A	209	16.666	12.506	32.852	1.00	11.42	C
ATOM	2940	O	SER	A	209	17.108	13.568	32.420	1.00	12.21	O
ATOM	2941	N	ARG	A	210	16.797	12.128	34.107	1.00	13.04	N
ATOM	2943	CA	ARG	A	210	17.480	12.973	35.089	1.00	12.02	C
ATOM	2945	CB	ARG	A	210	16.783	12.925	36.439	1.00	11.62	C
ATOM	2948	CG	ARG	A	210	15.644	13.914	36.659	1.00	10.95	C
ATOM	2951	CD	ARG	A	210	14.531	13.936	35.593	1.00	12.61	C
ATOM	2954	NE	ARG	A	210	13.496	14.936	35.948	1.00	13.59	N
ATOM	2956	CZ	ARG	A	210	12.450	15.250	35.214	1.00	14.23	C
ATOM	2957	NH1	ARG	A	210	12.267	14.655	34.035	1.00	14.26	N
ATOM	2960	NH2	ARG	A	210	11.550	16.168	35.652	1.00	13.18	N
ATOM	2963	C	ARG	A	210	18.906	12.544	35.328	1.00	11.40	C
ATOM	2964	O	ARG	A	210	19.201	11.401	35.281	1.00	12.42	O
ATOM	2965	N	GLY	A	211	19.756	13.520	35.625	1.00	13.31	N
ATOM	2967	CA	GLY	A	211	21.140	13.289	35.977	1.00	11.79	C
ATOM	2970	C	GLY	A	211	21.263	12.757	37.395	1.00	13.79	C
ATOM	2971	O	GLY	A	211	20.286	12.467	38.054	1.00	13.33	O
ATOM	2972	N	ASN	A	212	22.508	12.644	37.831	1.00	12.68	N
ATOM	2974	CA	ASN	A	212	22.852	12.132	39.139	1.00	13.86	C
ATOM	2976	CB	ASN	A	212	24.300	11.647	39.062	1.00	14.05	C
ATOM	2979	CG	ASN	A	212	24.801	11.076	40.380	1.00	15.77	C
ATOM	2980	OD1	ASN	A	212	24.034	10.961	41.330	1.00	20.22	O
ATOM	2981	ND2	ASN	A	212	26.057	10.638	40.402	1.00	21.14	N
ATOM	2984	C	ASN	A	212	22.711	13.289	40.154	1.00	13.72	C
ATOM	2985	O	ASN	A	212	23.466	14.254	40.141	1.00	13.40	O
ATOM	2986	N	PRO	A	213	21.803	13.173	41.121	1.00	14.98	N
ATOM	2987	CA	PRO	A	213	21.672	14.248	42.125	1.00	16.29	C
ATOM	2989	CB	PRO	A	213	20.586	13.722	43.065	1.00	17.58	C

ATOM	2992	CG	PRO	A	213	19.803	12.803	42.224	1.00	16.96	C
ATOM	2995	CD	PRO	A	213	20.863	12.072	41.386	1.00	15.73	C
ATOM	2998	C	PRO	A	213	22.966	14.577	42.864	1.00	16.46	C
ATOM	2999	O	PRO	A	213	23.194	15.766	43.089	1.00	18.16	O
ATOM	3000	N	ALA	A	214	23.809	13.573	43.084	1.00	17.81	N
ATOM	3002	CA	ALA	A	214	25.058	13.706	43.843	1.00	18.79	C
ATOM	3004	CB	ALA	A	214	25.746	12.336	44.004	1.00	19.37	C
ATOM	3008	C	ALA	A	214	26.022	14.653	43.188	1.00	18.92	C
ATOM	3009	O	ALA	A	214	26.872	15.225	43.890	1.00	17.86	O
ATOM	3010	N	THR	A	215	25.899	14.879	41.869	1.00	17.03	N
ATOM	3012	CA	THR	A	215	26.868	15.751	41.205	1.00	16.66	C
ATOM	3014	CB	THR	A	215	27.741	14.942	40.212	1.00	18.38	C
ATOM	3016	OG1	THR	A	215	26.907	14.218	39.271	1.00	15.43	O
ATOM	3018	CG2	THR	A	215	28.532	13.928	40.970	1.00	18.05	C
ATOM	3022	C	THR	A	215	26.278	16.952	40.479	1.00	16.40	C
ATOM	3023	O	THR	A	215	26.955	17.636	39.745	1.00	16.41	O
ATOM	3024	N	ALA	A	216	25.035	17.244	40.773	1.00	14.91	N
ATOM	3026	CA	ALA	A	216	24.408	18.446	40.249	1.00	16.14	C
ATOM	3028	CB	ALA	A	216	22.944	18.182	39.938	1.00	16.49	C
ATOM	3032	C	ALA	A	216	24.479	19.548	41.271	1.00	17.73	C
ATOM	3033	O	ALA	A	216	24.240	19.279	42.445	1.00	21.27	O
ATOM	3034	N	GLY	A	217	24.699	20.763	40.840	1.00	16.83	N
ATOM	3036	CA	GLY	A	217	24.701	21.920	41.725	1.00	17.35	C
ATOM	3039	C	GLY	A	217	25.994	22.704	41.603	1.00	18.14	C
ATOM	3040	O	GLY	A	217	26.068	23.906	41.983	1.00	19.91	O
ATOM	3041	N	ASP	A	218	27.007	22.103	41.001	1.00	17.40	N
ATOM	3043	CA	ASP	A	218	28.294	22.767	40.941	1.00	16.68	C
ATOM	3045	CB	ASP	A	218	29.346	21.732	41.259	1.00	17.36	C
ATOM	3048	CG	ASP	A	218	29.393	20.585	40.244	1.00	20.24	C
ATOM	3049	OD1	ASP	A	218	28.520	20.437	39.333	1.00	17.05	O
ATOM	3050	OD2	ASP	A	218	30.286	19.734	40.356	1.00	20.78	O
ATOM	3051	C	ASP	A	218	28.648	23.526	39.664	1.00	15.65	C
ATOM	3052	O	ASP	A	218	29.638	24.231	39.613	1.00	15.75	O
ATOM	3053	N	TYR	A	219	27.756	23.522	38.689	1.00	15.41	N
ATOM	3055	CA	TYR	A	219	28.003	24.099	37.380	1.00	13.99	C
ATOM	3057	CB	TYR	A	219	27.987	25.607	37.463	1.00	14.94	C
ATOM	3060	CG	TYR	A	219	26.611	26.197	37.674	1.00	15.83	C
ATOM	3061	CD1	TYR	A	219	25.642	26.086	36.702	1.00	12.98	C
ATOM	3063	CE1	TYR	A	219	24.385	26.648	36.871	1.00	12.57	C
ATOM	3065	CZ	TYR	A	219	24.125	27.301	38.052	1.00	18.74	C
ATOM	3066	OH	TYR	A	219	22.947	27.921	38.286	1.00	18.11	O
ATOM	3068	CE2	TYR	A	219	25.090	27.438	39.021	1.00	19.74	C
ATOM	3070	CD2	TYR	A	219	26.309	26.869	38.843	1.00	19.78	C
ATOM	3072	C	TYR	A	219	29.346	23.584	36.756	1.00	14.17	C
ATOM	3073	O	TYR	A	219	29.978	24.283	35.984	1.00	14.67	O
ATOM	3074	N	ILE	A	220	29.676	22.330	37.031	1.00	13.56	N
ATOM	3076	CA	ILE	A	220	30.775	21.624	36.414	1.00	15.58	C
ATOM	3078	CB	ILE	A	220	31.961	21.438	37.355	1.00	15.45	C
ATOM	3080	CG1	ILE	A	220	32.502	22.809	37.761	1.00	20.96	C
ATOM	3083	CD1	ILE	A	220	33.397	22.711	39.015	1.00	23.15	C
ATOM	3087	CG2	ILE	A	220	33.087	20.625	36.671	1.00	18.47	C
ATOM	3091	C	ILE	A	220	30.227	20.278	35.956	1.00	13.00	C
ATOM	3092	O	ILE	A	220	29.633	19.505	36.691	1.00	12.94	O
ATOM	3093	N	ILE	A	221	30.482	19.995	34.684	1.00	15.43	N
ATOM	3095	CA	ILE	A	221	29.934	18.782	34.088	1.00	13.93	C
ATOM	3097	CB	ILE	A	221	29.793	18.960	32.541	1.00	12.79	C
ATOM	3099	CG1	ILE	A	221	28.733	19.979	32.164	1.00	12.82	C
ATOM	3102	CD1	ILE	A	221	27.361	19.711	32.673	1.00	12.70	C

ATOM	3106	CG2	ILE	A	221	29.513	17.651	31.889	1.00	14.76	C
ATOM	3110	C	ILE	A	221	30.836	17.584	34.406	1.00	14.63	C
ATOM	3111	O	ILE	A	221	32.059	17.583	34.006	1.00	14.50	O
ATOM	3112	N	GLN	A	222	30.246	16.602	35.097	1.00	13.31	N
ATOM	3114	CA	GLN	A	222	30.786	15.267	35.285	1.00	14.28	C
ATOM	3116	CB	GLN	A	222	30.772	14.858	36.759	1.00	16.33	C
ATOM	3119	CG	GLN	A	222	31.775	15.669	37.602	1.00	18.83	C
ATOM	3122	CD	GLN	A	222	31.204	16.936	38.223	1.00	21.01	C
ATOM	3123	OE1	GLN	A	222	29.998	17.058	38.469	1.00	22.83	O
ATOM	3124	NE2	GLN	A	222	32.089	17.874	38.517	1.00	23.39	N
ATOM	3127	C	GLN	A	222	29.935	14.289	34.460	1.00	14.17	C
ATOM	3128	O	GLN	A	222	28.921	14.664	33.874	1.00	12.09	O
ATOM	3129	N	GLU	A	223	30.438	13.079	34.313	1.00	13.56	N
ATOM	3131	CA	GLU	A	223	29.646	12.052	33.675	1.00	14.32	C
ATOM	3133	CB	GLU	A	223	30.455	10.767	33.682	1.00	14.62	C
ATOM	3136	CG	GLU	A	223	29.787	9.618	32.984	1.00	15.34	C
ATOM	3139	CD	GLU	A	223	30.759	8.474	32.706	1.00	16.41	C
ATOM	3140	OE1	GLU	A	223	31.400	8.407	31.648	1.00	19.83	O
ATOM	3141	OE2	GLU	A	223	30.808	7.645	33.564	1.00	19.76	O
ATOM	3142	C	GLU	A	223	28.315	11.911	34.451	1.00	12.77	C
ATOM	3143	O	GLU	A	223	28.294	11.981	35.679	1.00	13.97	O
ATOM	3144	N	ARG	A	224	27.210	11.785	33.700	1.00	11.67	N
ATOM	3146	CA	ARG	A	224	25.834	11.585	34.178	1.00	11.39	C
ATOM	3148	CB	ARG	A	224	25.730	10.549	35.305	1.00	12.52	C
ATOM	3151	CG	ARG	A	224	26.269	9.156	34.960	1.00	16.20	C
ATOM	3154	CD	ARG	A	224	25.988	8.116	36.088	1.00	19.39	C
ATOM	3157	NE	ARG	A	224	24.589	7.737	36.052	1.00	19.97	N
ATOM	3159	CZ	ARG	A	224	24.123	6.785	35.271	1.00	23.20	C
ATOM	3160	NH1	ARG	A	224	24.939	6.070	34.516	1.00	22.67	N
ATOM	3163	NH2	ARG	A	224	22.835	6.530	35.234	1.00	20.20	N
ATOM	3166	C	ARG	A	224	25.199	12.934	34.600	1.00	11.27	C
ATOM	3167	O	ARG	A	224	24.137	12.954	35.247	1.00	12.76	O
ATOM	3168	N	ASP	A	225	25.779	14.065	34.167	1.00	10.64	N
ATOM	3170	CA	ASP	A	225	25.141	15.322	34.440	1.00	11.57	C
ATOM	3172	CB	ASP	A	225	26.137	16.421	34.763	1.00	12.18	C
ATOM	3175	CG	ASP	A	225	26.783	16.290	36.115	1.00	11.47	C
ATOM	3176	OD1	ASP	A	225	26.396	15.431	36.930	1.00	12.63	O
ATOM	3177	OD2	ASP	A	225	27.738	17.024	36.366	1.00	12.98	O
ATOM	3178	C	ASP	A	225	24.386	15.833	33.187	1.00	11.72	C
ATOM	3179	O	ASP	A	225	24.880	15.761	32.028	1.00	10.65	O
ATOM	3180	N	ILE	A	226	23.195	16.366	33.428	1.00	10.89	N
ATOM	3182	CA	ILE	A	226	22.449	17.089	32.399	1.00	10.95	C
ATOM	3184	CB	ILE	A	226	20.988	17.379	32.826	1.00	10.97	C
ATOM	3186	CG1	ILE	A	226	20.296	16.066	33.224	1.00	8.65	C
ATOM	3189	CD1	ILE	A	226	20.064	15.192	32.004	1.00	12.39	C
ATOM	3193	CG2	ILE	A	226	20.260	18.217	31.828	1.00	12.31	C
ATOM	3197	C	ILE	A	226	23.117	18.428	32.195	1.00	8.74	C
ATOM	3198	O	ILE	A	226	23.561	19.076	33.123	1.00	10.81	O
ATOM	3199	N	GLU	A	227	23.254	18.849	30.971	1.00	9.24	N
ATOM	3201	CA	GLU	A	227	23.902	20.150	30.715	1.00	9.53	C
ATOM	3203	CB	GLU	A	227	24.905	19.979	29.553	1.00	8.94	C
ATOM	3206	CG	GLU	A	227	25.869	21.131	29.345	1.00	9.79	C
ATOM	3209	CD	GLU	A	227	27.217	20.634	28.789	1.00	11.40	C
ATOM	3210	OE1	GLU	A	227	27.527	19.431	28.857	1.00	8.56	O
ATOM	3211	OE2	GLU	A	227	27.953	21.441	28.255	1.00	11.05	O
ATOM	3212	C	GLU	A	227	22.936	21.331	30.450	1.00	9.10	C
ATOM	3213	O	GLU	A	227	23.053	22.402	31.074	1.00	10.35	O
ATOM	3214	N	VAL	A	228	21.984	21.152	29.553	1.00	8.61	N

ATOM	3216	CA	VAL	A	228	21.094	22.222	29.176	1.00	7.54	C
ATOM	3218	CB	VAL	A	228	21.567	23.010	27.946	1.00	5.96	C
ATOM	3220	CG1	VAL	A	228	22.834	23.726	28.263	1.00	8.28	C
ATOM	3224	CG2	VAL	A	228	21.680	22.127	26.740	1.00	8.08	C
ATOM	3228	C	VAL	A	228	19.727	21.575	28.904	1.00	7.83	C
ATOM	3229	O	VAL	A	228	19.663	20.362	28.747	1.00	9.43	O
ATOM	3230	N	SER	A	229	18.716	22.426	28.809	1.00	10.13	N
ATOM	3232	CA	SER	A	229	17.369	22.024	28.520	1.00	9.88	C
ATOM	3234	CB	SER	A	229	16.457	22.371	29.674	1.00	10.86	C
ATOM	3237	OG	SER	A	229	16.811	21.670	30.827	1.00	11.90	O
ATOM	3239	C	SER	A	229	16.865	22.806	27.305	1.00	11.07	C
ATOM	3240	O	SER	A	229	17.290	23.949	27.065	1.00	11.59	O
ATOM	3241	N	ALA	A	230	15.964	22.167	26.536	1.00	10.22	N
ATOM	3243	CA	ALA	A	230	15.337	22.824	25.379	1.00	9.98	C
ATOM	3245	CB	ALA	A	230	16.245	22.786	24.202	1.00	11.98	C
ATOM	3249	C	ALA	A	230	14.001	22.181	25.011	1.00	10.40	C
ATOM	3250	O	ALA	A	230	13.639	21.143	25.539	1.00	11.74	O
ATOM	3251	N	PRO	A	231	13.241	22.873	24.162	1.00	12.52	N
ATOM	3252	CA	PRO	A	231	11.915	22.369	23.794	1.00	11.45	C
ATOM	3254	CB	PRO	A	231	11.440	23.308	22.676	1.00	12.82	C
ATOM	3257	CG	PRO	A	231	12.076	24.609	23.005	1.00	12.47	C
ATOM	3260	CD	PRO	A	231	13.518	24.184	23.540	1.00	12.90	C
ATOM	3263	C	PRO	A	231	11.967	20.969	23.241	1.00	10.90	C
ATOM	3264	O	PRO	A	231	12.689	20.713	22.238	1.00	11.39	O
ATOM	3265	N	GLY	A	232	11.194	20.071	23.863	1.00	11.69	N
ATOM	3267	CA	GLY	A	232	11.218	18.675	23.478	1.00	12.12	C
ATOM	3270	C	GLY	A	232	9.857	17.972	23.431	1.00	14.63	C
ATOM	3271	O	GLY	A	232	9.814	16.852	22.976	1.00	17.38	O
ATOM	3272	N	ALA	A	233	8.775	18.641	23.807	1.00	13.80	N
ATOM	3274	CA	ALA	A	233	7.441	17.975	23.841	1.00	15.69	C
ATOM	3276	CB	ALA	A	233	6.812	18.002	25.228	1.00	15.50	C
ATOM	3280	C	ALA	A	233	6.565	18.649	22.794	1.00	15.70	C
ATOM	3281	O	ALA	A	233	6.479	19.892	22.725	1.00	15.71	O
ATOM	3282	N	SER	A	234	6.008	17.837	21.901	1.00	15.70	N
ATOM	3284	CA	SER	A	234	5.123	18.323	20.820	1.00	17.34	C
ATOM	3286	CB	SER	A	234	3.816	18.866	21.396	1.00	19.34	C
ATOM	3289	OG	SER	A	234	3.151	17.862	22.071	1.00	24.09	O
ATOM	3291	C	SER	A	234	5.746	19.302	19.869	1.00	16.08	C
ATOM	3292	O	SER	A	234	5.311	20.419	19.727	1.00	16.37	O
ATOM	3293	N	VAL	A	235	6.816	18.859	19.244	1.00	13.70	N
ATOM	3295	CA	VAL	A	235	7.597	19.607	18.309	1.00	13.30	C
ATOM	3297	CB	VAL	A	235	9.124	19.358	18.536	1.00	11.29	C
ATOM	3299	CG1	VAL	A	235	9.948	19.994	17.533	1.00	11.79	C
ATOM	3303	CG2	VAL	A	235	9.475	19.925	19.919	1.00	13.78	C
ATOM	3307	C	VAL	A	235	7.284	19.242	16.876	1.00	14.46	C
ATOM	3308	O	VAL	A	235	7.529	18.141	16.413	1.00	15.04	O
ATOM	3309	N	GLU	A	236	6.773	20.208	16.151	1.00	15.81	N
ATOM	3311	CA	GLU	A	236	6.539	20.075	14.717	1.00	15.96	C
ATOM	3313	CB	GLU	A	236	5.419	21.059	14.323	1.00	16.03	C
ATOM	3316	CG	GLU	A	236	5.033	21.028	12.863	1.00	18.99	C
ATOM	3319	CD	GLU	A	236	3.833	21.939	12.549	1.00	22.94	C
ATOM	3320	OE1	GLU	A	236	3.422	22.715	13.457	1.00	20.60	O
ATOM	3321	OE2	GLU	A	236	3.255	21.772	11.420	1.00	20.10	O
ATOM	3322	C	GLU	A	236	7.751	20.349	13.881	1.00	16.01	C
ATOM	3323	O	GLU	A	236	8.534	21.272	14.139	1.00	17.39	O
ATOM	3324	N	SER	A	237	8.023	19.462	12.905	1.00	14.14	N
ATOM	3326	CA	SER	A	237	9.105	19.655	12.025	1.00	14.47	C
ATOM	3328	CB	SER	A	237	10.410	19.109	12.632	1.00	11.88	C

ATOM	3331	OG	SER	A	237	11.513	19.504	11.921	1.00	11.55	O
ATOM	3333	C	SER	A	237	8.819	18.900	10.715	1.00	14.97	C
ATOM	3334	O	SER	A	237	7.699	18.345	10.543	1.00	16.60	O
ATOM	3335	N	THR	A	238	9.838	18.892	9.886	1.00	15.64	N
ATOM	3337	CA	THR	A	238	9.851	18.230	8.581	1.00	17.00	C
ATOM	3339	CB	THR	A	238	11.090	18.559	7.844	1.00	18.10	C
ATOM	3341	OG1	THR	A	238	12.267	18.454	8.677	1.00	16.55	O
ATOM	3343	CG2	THR	A	238	11.152	19.996	7.339	1.00	16.33	C
ATOM	3347	C	THR	A	238	9.752	16.703	8.759	1.00	19.28	C
ATOM	3348	O	THR	A	238	10.213	16.169	9.768	1.00	18.16	O
ATOM	3349	N	TRP	A	239	9.203	16.032	7.739	1.00	19.48	N
ATOM	3351	CA	TRP	A	239	8.933	14.587	7.765	1.00	18.83	C
ATOM	3353	CB	TRP	A	239	7.503	14.322	8.122	1.00	19.25	C
ATOM	3356	CG	TRP	A	239	7.182	12.954	8.642	1.00	19.71	C
ATOM	3357	CD1	TRP	A	239	6.343	12.009	8.085	1.00	23.51	C
ATOM	3359	NE1	TRP	A	239	6.263	10.907	8.899	1.00	22.49	N
ATOM	3361	CE2	TRP	A	239	7.081	11.114	9.985	1.00	21.32	C
ATOM	3362	CD2	TRP	A	239	7.651	12.400	9.853	1.00	20.74	C
ATOM	3363	CE3	TRP	A	239	8.529	12.864	10.851	1.00	18.32	C
ATOM	3365	CZ3	TRP	A	239	8.751	12.055	11.962	1.00	21.08	C
ATOM	3367	CH2	TRP	A	239	8.166	10.788	12.061	1.00	20.53	C
ATOM	3369	CZ2	TRP	A	239	7.349	10.289	11.079	1.00	22.21	C
ATOM	3371	C	TRP	A	239	9.325	13.931	6.461	1.00	17.68	C
ATOM	3372	O	TRP	A	239	9.417	14.577	5.423	1.00	19.48	O
ATOM	3373	N	TYR	A	240	9.679	12.642	6.550	1.00	17.80	N
ATOM	3375	CA	TYR	A	240	10.332	11.947	5.485	1.00	17.76	C
ATOM	3377	CB	TYR	A	240	10.862	10.568	5.938	1.00	20.08	C
ATOM	3380	CG	TYR	A	240	9.864	9.469	6.036	1.00	17.92	C
ATOM	3381	CD1	TYR	A	240	8.997	9.367	7.097	1.00	20.96	C
ATOM	3383	CE1	TYR	A	240	8.113	8.325	7.179	1.00	22.25	C
ATOM	3385	CZ	TYR	A	240	8.150	7.317	6.171	1.00	27.67	C
ATOM	3386	OH	TYR	A	240	7.269	6.247	6.207	1.00	28.63	O
ATOM	3388	CE2	TYR	A	240	9.034	7.397	5.159	1.00	25.36	C
ATOM	3390	CD2	TYR	A	240	9.884	8.442	5.084	1.00	24.19	C
ATOM	3392	C	TYR	A	240	9.453	11.746	4.253	1.00	19.14	C
ATOM	3393	O	TYR	A	240	9.992	11.532	3.199	1.00	19.72	O
ATOM	3394	N	THR	A	241	8.172	11.873	4.401	1.00	21.32	N
ATOM	3396	CA	THR	A	241	7.309	11.777	3.214	1.00	24.31	C
ATOM	3398	CB	THR	A	241	6.015	11.129	3.549	1.00	24.08	C
ATOM	3400	OG1	THR	A	241	5.443	11.711	4.720	1.00	25.38	O
ATOM	3402	CG2	THR	A	241	6.238	9.670	3.924	1.00	28.14	C
ATOM	3406	C	THR	A	241	7.020	13.113	2.587	1.00	26.01	C
ATOM	3407	O	THR	A	241	6.175	13.200	1.682	1.00	27.85	O
ATOM	3408	N	GLY	A	242	7.684	14.159	3.041	1.00	26.13	N
ATOM	3410	CA	GLY	A	242	7.445	15.480	2.484	1.00	26.65	C
ATOM	3413	C	GLY	A	242	6.544	16.381	3.303	1.00	25.41	C
ATOM	3414	O	GLY	A	242	6.524	17.583	3.068	1.00	29.27	O
ATOM	3415	N	GLY	A	243	5.786	15.891	4.246	1.00	23.67	N
ATOM	3417	CA	GLY	A	243	5.002	16.882	4.959	1.00	23.78	C
ATOM	3420	C	GLY	A	243	5.719	17.300	6.239	1.00	21.57	C
ATOM	3421	O	GLY	A	243	6.944	17.532	6.218	1.00	20.45	O
ATOM	3422	N	TYR	A	244	4.939	17.380	7.296	1.00	22.18	N
ATOM	3424	CA	TYR	A	244	5.404	17.745	8.651	1.00	21.26	C
ATOM	3426	CB	TYR	A	244	4.991	19.201	8.963	1.00	20.92	C
ATOM	3429	CG	TYR	A	244	5.467	20.078	7.877	1.00	20.48	C
ATOM	3430	CD1	TYR	A	244	4.696	20.312	6.749	1.00	20.98	C
ATOM	3432	CE1	TYR	A	244	5.167	21.082	5.733	1.00	21.20	C
ATOM	3434	CZ	TYR	A	244	6.396	21.604	5.785	1.00	20.81	C

ATOM	3435	OH	TYR	A	244	6.852	22.332	4.745	1.00	23.64	O
ATOM	3437	CE2	TYR	A	244	7.201	21.392	6.929	1.00	17.10	C
ATOM	3439	CD2	TYR	A	244	6.714	20.660	7.920	1.00	14.54	C
ATOM	3441	C	TYR	A	244	4.789	16.816	9.621	1.00	21.28	C
ATOM	3442	O	TYR	A	244	3.778	16.224	9.353	1.00	23.43	O
ATOM	3443	N	ASN	A	245	5.381	16.692	10.800	1.00	19.64	N
ATOM	3445	CA	ASN	A	245	4.866	15.855	11.825	1.00	18.70	C
ATOM	3447	CB	ASN	A	245	5.322	14.418	11.590	1.00	18.51	C
ATOM	3450	CG	ASN	A	245	4.644	13.438	12.450	1.00	18.67	C
ATOM	3451	OD1	ASN	A	245	3.509	13.611	12.925	1.00	21.26	O
ATOM	3452	ND2	ASN	A	245	5.350	12.323	12.689	1.00	22.00	N
ATOM	3455	C	ASN	A	245	5.304	16.401	13.154	1.00	16.91	C
ATOM	3456	O	ASN	A	245	6.289	17.194	13.212	1.00	17.80	O
ATOM	3457	N	THR	A	246	4.533	16.035	14.141	1.00	17.22	N
ATOM	3459	CA	THR	A	246	4.696	16.445	15.504	1.00	17.23	C
ATOM	3461	CB	THR	A	246	3.454	17.242	15.971	1.00	17.67	C
ATOM	3463	OG1	THR	A	246	3.368	18.458	15.223	1.00	18.24	O
ATOM	3465	CG2	THR	A	246	3.534	17.710	17.400	1.00	20.37	C
ATOM	3469	C	THR	A	246	4.993	15.244	16.374	1.00	17.33	C
ATOM	3470	O	THR	A	246	4.123	14.398	16.664	1.00	16.60	O
ATOM	3471	N	ILE	A	247	6.221	15.237	16.902	1.00	16.92	N
ATOM	3473	CA	ILE	A	247	6.655	14.201	17.813	1.00	16.77	C
ATOM	3475	CB	ILE	A	247	7.536	13.106	17.091	1.00	16.85	C
ATOM	3477	CG1	ILE	A	247	8.722	13.699	16.372	1.00	16.22	C
ATOM	3480	CD1	ILE	A	247	9.721	12.674	15.892	1.00	14.19	C
ATOM	3484	CG2	ILE	A	247	6.620	12.272	16.155	1.00	18.78	C
ATOM	3488	C	ILE	A	247	7.394	14.839	19.045	1.00	14.93	C
ATOM	3489	O	ILE	A	247	7.628	16.050	19.098	1.00	15.83	O
ATOM	3490	N	SER	A	248	7.659	14.020	20.030	1.00	14.46	N
ATOM	3492	CA	SER	A	248	8.268	14.443	21.285	1.00	14.38	C
ATOM	3494	CB	SER	A	248	7.262	14.230	22.426	1.00	14.68	C
ATOM	3497	OG	SER	A	248	6.080	14.988	22.271	1.00	16.96	O
ATOM	3499	C	SER	A	248	9.470	13.594	21.672	1.00	13.40	C
ATOM	3500	O	SER	A	248	9.626	12.448	21.227	1.00	12.06	O
ATOM	3501	N	GLY	A	249	10.306	14.151	22.557	1.00	11.90	N
ATOM	3503	CA	GLY	A	249	11.402	13.420	23.140	1.00	12.25	C
ATOM	3506	C	GLY	A	249	12.615	14.294	23.393	1.00	11.45	C
ATOM	3507	O	GLY	A	249	12.672	15.399	22.898	1.00	12.12	O
ATOM	3508	N	THR	A	250	13.607	13.759	24.103	1.00	10.99	N
ATOM	3510	CA	THR	A	250	14.898	14.476	24.200	1.00	9.84	C
ATOM	3512	CB	THR	A	250	15.835	13.937	25.257	1.00	9.57	C
ATOM	3514	OG1	THR	A	250	15.885	12.543	25.195	1.00	10.83	O
ATOM	3516	CG2	THR	A	250	15.260	14.258	26.612	1.00	11.12	C
ATOM	3520	C	THR	A	250	15.506	14.531	22.800	1.00	9.75	C
ATOM	3521	O	THR	A	250	16.312	15.393	22.517	1.00	11.31	O
ATOM	3522	N	SER	A	251	15.101	13.616	21.938	1.00	9.71	N
ATOM	3524	CA	SER	A	251	15.396	13.711	20.513	1.00	10.29	C
ATOM	3526	CB	SER	A	251	14.647	12.660	19.691	1.00	10.44	C
ATOM	3529	OG	SER	A	251	15.278	11.374	19.720	1.00	11.64	O
ATOM	3531	C	SER	A	251	15.132	15.058	19.850	1.00	10.60	C
ATOM	3532	O	SER	A	251	15.871	15.475	18.968	1.00	12.05	O
ATOM	3533	N	MET	A	252	14.023	15.698	20.246	1.00	11.35	N
ATOM	3535	CA	MET	A	252	13.598	16.937	19.649	1.00	12.05	C
ATOM	3537	CB	MET	A	252	12.081	17.000	19.803	1.00	10.74	C
ATOM	3540	CG	MET	A	252	11.275	16.163	18.811	1.00	16.05	C
ATOM	3543	SD	MET	A	252	11.445	14.393	18.855	1.00	12.67	S
ATOM	3544	CE	MET	A	252	12.360	14.105	17.508	1.00	14.70	C
ATOM	3548	C	MET	A	252	14.248	18.146	20.363	1.00	11.00	C

ATOM	3549	O	MET	A	252	14.372	19.200	19.805	1.00	10.97	O
ATOM	3550	N	ALA	A	253	14.615	17.978	21.628	1.00	11.44	N
ATOM	3552	CA	ALA	A	253	15.300	19.023	22.361	1.00	9.30	C
ATOM	3554	CB	ALA	A	253	15.282	18.677	23.852	1.00	8.63	C
ATOM	3558	C	ALA	A	253	16.733	19.234	21.842	1.00	9.29	C
ATOM	3559	O	ALA	A	253	17.173	20.367	21.599	1.00	10.72	O
ATOM	3560	N	THR	A	254	17.388	18.107	21.578	1.00	9.20	N
ATOM	3562	CA	THR	A	254	18.776	18.047	21.127	1.00	9.63	C
ATOM	3564	CB	THR	A	254	19.131	16.592	20.838	1.00	11.67	C
ATOM	3566	OG1	THR	A	254	19.001	15.823	22.036	1.00	9.34	O
ATOM	3568	CG2	THR	A	254	20.504	16.467	20.434	1.00	9.85	C
ATOM	3572	C	THR	A	254	19.041	18.957	19.927	1.00	9.01	C
ATOM	3573	O	THR	A	254	19.932	19.782	19.958	1.00	9.02	O
ATOM	3574	N	PRO	A	255	18.255	18.848	18.856	1.00	10.43	N
ATOM	3575	CA	PRO	A	255	18.491	19.725	17.711	1.00	9.72	C
ATOM	3577	CB	PRO	A	255	17.607	19.149	16.621	1.00	11.04	C
ATOM	3580	CG	PRO	A	255	16.511	18.430	17.368	1.00	11.23	C
ATOM	3583	CD	PRO	A	255	17.253	17.817	18.535	1.00	11.38	C
ATOM	3586	C	PRO	A	255	18.195	21.185	17.941	1.00	10.12	C
ATOM	3587	O	PRO	A	255	18.724	22.018	17.171	1.00	9.83	O
ATOM	3588	N	HIS	A	256	17.398	21.535	18.943	1.00	10.53	N
ATOM	3590	CA	HIS	A	256	17.233	22.947	19.219	1.00	10.79	C
ATOM	3592	CB	HIS	A	256	16.192	23.258	20.298	1.00	11.66	C
ATOM	3595	CG	HIS	A	256	14.748	23.136	19.820	1.00	12.48	C
ATOM	3596	ND1	HIS	A	256	14.086	21.930	19.732	1.00	11.32	N
ATOM	3598	CE1	HIS	A	256	12.849	22.144	19.296	1.00	14.50	C
ATOM	3600	NE2	HIS	A	256	12.709	23.434	19.040	1.00	12.79	N
ATOM	3602	CD2	HIS	A	256	13.889	24.074	19.348	1.00	12.20	C
ATOM	3604	C	HIS	A	256	18.572	23.451	19.658	1.00	11.12	C
ATOM	3605	O	HIS	A	256	18.977	24.554	19.302	1.00	12.50	O
ATOM	3606	N	VAL	A	257	19.264	22.660	20.474	1.00	10.13	N
ATOM	3608	CA	VAL	A	257	20.558	23.078	20.969	1.00	9.71	C
ATOM	3610	CB	VAL	A	257	20.966	22.264	22.219	1.00	10.12	C
ATOM	3612	CG1	VAL	A	257	22.407	22.589	22.653	1.00	10.84	C
ATOM	3616	CG2	VAL	A	257	19.951	22.451	23.324	1.00	11.41	C
ATOM	3620	C	VAL	A	257	21.632	22.993	19.871	1.00	10.99	C
ATOM	3621	O	VAL	A	257	22.483	23.871	19.782	1.00	11.55	O
ATOM	3622	N	ALA	A	258	21.664	21.933	19.070	1.00	10.95	N
ATOM	3624	CA	ALA	A	258	22.625	21.857	17.985	1.00	10.24	C
ATOM	3626	CB	ALA	A	258	22.459	20.568	17.233	1.00	9.96	C
ATOM	3630	C	ALA	A	258	22.446	23.027	17.061	1.00	11.33	C
ATOM	3631	O	ALA	A	258	23.426	23.621	16.598	1.00	10.81	O
ATOM	3632	N	GLY	A	259	21.191	23.351	16.799	1.00	11.66	N
ATOM	3634	CA	GLY	A	259	20.929	24.467	15.916	1.00	12.69	C
ATOM	3637	C	GLY	A	259	21.378	25.792	16.529	1.00	11.32	C
ATOM	3638	O	GLY	A	259	21.928	26.653	15.830	1.00	12.25	O
ATOM	3639	N	LEU	A	260	21.044	25.991	17.781	1.00	10.90	N
ATOM	3641	CA	LEU	A	260	21.453	27.191	18.479	1.00	11.40	C
ATOM	3643	CB	LEU	A	260	20.945	27.240	19.877	1.00	10.96	C
ATOM	3646	CG	LEU	A	260	21.372	28.483	20.678	1.00	11.84	C
ATOM	3648	CD1	LEU	A	260	20.781	29.683	20.099	1.00	16.22	C
ATOM	3652	CD2	LEU	A	260	20.948	28.349	22.174	1.00	12.84	C
ATOM	3656	C	LEU	A	260	22.984	27.291	18.477	1.00	12.53	C
ATOM	3657	O	LEU	A	260	23.558	28.384	18.205	1.00	11.28	O
ATOM	3658	N	ALA	A	261	23.644	26.153	18.745	1.00	11.39	N
ATOM	3660	CA	ALA	A	261	25.093	26.133	18.661	1.00	11.97	C
ATOM	3662	CB	ALA	A	261	25.604	24.716	18.889	1.00	13.65	C
ATOM	3666	C	ALA	A	261	25.607	26.638	17.292	1.00	12.95	C

ATOM	3667	O	ALA	A	261	26.563	27.413	17.203	1.00	12.12	O
ATOM	3668	N	ALA	A	262	24.998	26.144	16.229	1.00	11.02	N
ATOM	3670	CA	ALA	A	262	25.435	26.520	14.869	1.00	12.24	C
ATOM	3672	CB	ALA	A	262	24.731	25.669	13.828	1.00	12.25	C
ATOM	3676	C	ALA	A	262	25.200	28.002	14.619	1.00	13.52	C
ATOM	3677	O	ALA	A	262	26.045	28.684	13.996	1.00	13.55	O
ATOM	3678	N	LYS	A	263	24.091	28.505	15.135	1.00	13.42	N
ATOM	3680	CA	LYS	A	263	23.730	29.913	15.021	1.00	13.54	C
ATOM	3682	CB	LYS	A	263	22.319	30.164	15.511	1.00	14.20	C
ATOM	3685	CG	LYS	A	263	21.797	31.603	15.356	1.00	13.78	C
ATOM	3688	CD	LYS	A	263	20.412	31.725	15.984	1.00	15.37	C
ATOM	3691	CE	LYS	A	263	19.936	33.158	16.011	1.00	17.70	C
ATOM	3694	NZ	LYS	A	263	19.671	33.740	14.618	1.00	14.92	N
ATOM	3698	C	LYS	A	263	24.754	30.774	15.736	1.00	12.81	C
ATOM	3699	O	LYS	A	263	25.225	31.781	15.148	1.00	13.25	O
ATOM	3700	N	ILE	A	264	25.133	30.393	16.961	1.00	12.96	N
ATOM	3702	CA	ILE	A	264	26.107	31.136	17.723	1.00	12.47	C
ATOM	3704	CB	ILE	A	264	26.209	30.579	19.150	1.00	12.83	C
ATOM	3706	CG1	ILE	A	264	24.895	30.799	19.927	1.00	12.96	C
ATOM	3709	CD1	ILE	A	264	24.829	30.017	21.259	1.00	13.94	C
ATOM	3713	CG2	ILE	A	264	27.382	31.146	19.925	1.00	12.54	C
ATOM	3717	C	ILE	A	264	27.478	31.081	17.018	1.00	12.78	C
ATOM	3718	O	ILE	A	264	28.147	32.110	16.835	1.00	12.72	O
ATOM	3719	N	TRP	A	265	27.843	29.890	16.527	1.00	12.74	N
ATOM	3721	CA	TRP	A	265	29.194	29.711	15.984	1.00	13.37	C
ATOM	3723	CB	TRP	A	265	29.445	28.252	15.665	1.00	13.60	C
ATOM	3726	CG	TRP	A	265	30.859	27.836	15.758	1.00	12.37	C
ATOM	3727	CD1	TRP	A	265	31.987	28.624	15.964	1.00	12.89	C
ATOM	3729	NE1	TRP	A	265	33.101	27.823	16.063	1.00	14.49	N
ATOM	3731	CE2	TRP	A	265	32.705	26.514	15.998	1.00	16.16	C
ATOM	3732	CD2	TRP	A	265	31.313	26.493	15.796	1.00	12.95	C
ATOM	3733	CE3	TRP	A	265	30.679	25.254	15.657	1.00	14.36	C
ATOM	3735	CZ3	TRP	A	265	31.472	24.110	15.707	1.00	12.68	C
ATOM	3737	CH2	TRP	A	265	32.809	24.180	15.941	1.00	12.39	C
ATOM	3739	CZ2	TRP	A	265	33.462	25.359	16.069	1.00	15.97	C
ATOM	3741	C	TRP	A	265	29.378	30.560	14.732	1.00	13.71	C
ATOM	3742	O	TRP	A	265	30.423	31.117	14.530	1.00	17.12	O
ATOM	3743	N	SER	A	266	28.330	30.599	13.922	1.00	15.25	N
ATOM	3745	CA	SER	A	266	28.307	31.345	12.676	1.00	14.75	C
ATOM	3747	CB	SER	A	266	27.000	31.130	11.945	1.00	15.47	C
ATOM	3750	OG	SER	A	266	26.987	31.917	10.741	1.00	18.19	O
ATOM	3752	C	SER	A	266	28.498	32.835	12.962	1.00	16.77	C
ATOM	3753	O	SER	A	266	29.218	33.537	12.227	1.00	16.07	O
ATOM	3754	N	ALA	A	267	27.903	33.307	14.053	1.00	15.63	N
ATOM	3756	CA	ALA	A	267	28.046	34.711	14.450	1.00	17.65	C
ATOM	3758	CB	ALA	A	267	26.911	35.093	15.318	1.00	19.01	C
ATOM	3762	C	ALA	A	267	29.405	35.056	15.092	1.00	19.17	C
ATOM	3763	O	ALA	A	267	29.744	36.249	15.277	1.00	18.66	O
ATOM	3764	N	ASN	A	268	30.188	34.053	15.465	1.00	17.88	N
ATOM	3766	CA	ASN	A	268	31.557	34.318	15.886	1.00	20.05	C
ATOM	3768	CB	ASN	A	268	31.688	34.603	17.324	1.00	20.47	C
ATOM	3771	CG	ASN	A	268	33.120	35.029	17.701	1.00	23.58	C
ATOM	3772	OD1	ASN	A	268	34.017	35.076	16.860	1.00	24.59	O
ATOM	3773	ND2	ASN	A	268	33.327	35.286	18.961	1.00	27.93	N
ATOM	3776	C	ASN	A	268	32.437	33.156	15.520	1.00	18.98	C
ATOM	3777	O	ASN	A	268	32.651	32.264	16.321	1.00	17.09	O
ATOM	3778	N	THR	A	269	32.915	33.169	14.289	1.00	19.21	N
ATOM	3780	CA	THR	A	269	33.696	32.076	13.772	1.00	19.25	C

ATOM	3782	CB	THR	A	269	33.838	32.153	12.207	1.00	21.27	C
ATOM	3784	OG1	THR	A	269	34.379	33.443	11.889	1.00	21.88	O
ATOM	3786	CG2	THR	A	269	32.479	32.127	11.565	1.00	23.50	C
ATOM	3790	C	THR	A	269	35.055	32.025	14.380	1.00	19.11	C
ATOM	3791	O	THR	A	269	35.761	31.117	14.072	1.00	19.77	O
ATOM	3792	N	SER	A	270	35.435	32.929	15.297	1.00	19.17	N
ATOM	3794	CA	SER	A	270	36.732	32.774	15.936	1.00	19.54	C
ATOM	3796	CB	ASER	A	270	37.231	34.105	16.454	0.50	19.48	C
ATOM	3797	CB	BSER	A	270	37.264	34.116	16.400	0.50	19.66	C
ATOM	3802	OG	ASER	A	270	36.235	34.749	17.225	0.50	21.34	O
ATOM	3803	OG	BSER	A	270	37.628	34.922	15.280	0.50	22.88	O
ATOM	3806	C	SER	A	270	36.679	31.795	17.100	1.00	17.42	C
ATOM	3807	O	SER	A	270	37.688	31.382	17.637	1.00	19.69	O
ATOM	3808	N	LEU	A	271	35.493	31.392	17.484	1.00	15.84	N
ATOM	3810	CA	LEU	A	271	35.364	30.456	18.595	1.00	13.46	C
ATOM	3812	CB	LEU	A	271	33.910	30.345	19.026	1.00	14.65	C
ATOM	3815	CG	LEU	A	271	33.146	31.575	19.466	1.00	15.68	C
ATOM	3817	CD1	LEU	A	271	31.659	31.196	19.782	1.00	18.69	C
ATOM	3821	CD2	LEU	A	271	33.807	32.216	20.685	1.00	21.20	C
ATOM	3825	C	LEU	A	271	35.806	29.028	18.220	1.00	12.04	C
ATOM	3826	O	LEU	A	271	35.573	28.546	17.091	1.00	11.86	O
ATOM	3827	N	SER	A	272	36.323	28.335	19.220	1.00	12.57	N
ATOM	3829	CA	SER	A	272	36.545	26.919	19.145	1.00	11.98	C
ATOM	3831	CB	SER	A	272	37.710	26.489	20.040	1.00	12.49	C
ATOM	3834	OG	SER	A	272	37.433	26.778	21.421	1.00	12.53	O
ATOM	3836	C	SER	A	272	35.275	26.244	19.663	1.00	11.47	C
ATOM	3837	O	SER	A	272	34.372	26.889	20.269	1.00	9.92	O
ATOM	3838	N	HIS	A	273	35.225	24.937	19.454	1.00	11.48	N
ATOM	3840	CA	HIS	A	273	34.074	24.187	19.920	1.00	11.75	C
ATOM	3842	CB	HIS	A	273	34.187	22.750	19.445	1.00	13.59	C
ATOM	3845	CG	HIS	A	273	35.160	21.921	20.197	1.00	13.01	C
ATOM	3846	ND1	HIS	A	273	36.456	22.312	20.379	1.00	11.73	N
ATOM	3848	CE1	HIS	A	273	37.072	21.402	21.124	1.00	13.52	C
ATOM	3850	NE2	HIS	A	273	36.243	20.394	21.343	1.00	12.58	N
ATOM	3852	CD2	HIS	A	273	35.039	20.708	20.787	1.00	14.38	C
ATOM	3854	C	HIS	A	273	33.887	24.268	21.427	1.00	11.79	C
ATOM	3855	O	HIS	A	273	32.723	24.252	21.930	1.00	10.83	O
ATOM	3856	N	SER	A	274	34.975	24.276	22.191	1.00	10.50	N
ATOM	3858	CA	SER	A	274	34.813	24.319	23.643	1.00	10.49	C
ATOM	3860	CB	SER	A	274	36.035	23.803	24.397	1.00	13.18	C
ATOM	3863	OG	SER	A	274	37.161	24.639	24.166	1.00	12.23	O
ATOM	3865	C	SER	A	274	34.478	25.702	24.113	1.00	12.50	C
ATOM	3866	O	SER	A	274	33.783	25.849	25.123	1.00	11.08	O
ATOM	3867	N	GLN	A	275	34.919	26.739	23.418	1.00	11.42	N
ATOM	3869	CA	GLN	A	275	34.425	28.072	23.784	1.00	11.21	C
ATOM	3871	CB	GLN	A	275	35.132	29.188	22.999	1.00	11.23	C
ATOM	3874	CG	GLN	A	275	36.608	29.464	23.375	1.00	13.15	C
ATOM	3877	CD	GLN	A	275	37.192	30.473	22.413	1.00	13.10	C
ATOM	3878	OE1	GLN	A	275	37.323	30.182	21.228	1.00	15.35	O
ATOM	3879	NE2	GLN	A	275	37.555	31.677	22.923	1.00	11.91	N
ATOM	3882	C	GLN	A	275	32.898	28.177	23.457	1.00	11.10	C
ATOM	3883	O	GLN	A	275	32.150	28.776	24.217	1.00	10.23	O
ATOM	3884	N	LEU	A	276	32.492	27.556	22.340	1.00	10.08	N
ATOM	3886	CA	LEU	A	276	31.067	27.521	21.932	1.00	10.49	C
ATOM	3888	CB	LEU	A	276	30.909	26.866	20.582	1.00	10.65	C
ATOM	3891	CG	LEU	A	276	29.466	26.606	20.164	1.00	8.36	C
ATOM	3893	CD1	LEU	A	276	28.715	27.856	20.038	1.00	9.01	C
ATOM	3897	CD2	LEU	A	276	29.489	25.869	18.849	1.00	11.63	C

ATOM	3901	C	LEU	A	276	30.272	26.790	23.041	1.00	11.06	C
ATOM	3902	O	LEU	A	276	29.226	27.252	23.494	1.00	10.87	O
ATOM	3903	N	ARG	A	277	30.783	25.671	23.524	1.00	9.13	N
ATOM	3905	CA	ARG	A	277	30.104	24.934	24.560	1.00	11.95	C
ATOM	3907	CB	ARG	A	277	30.915	23.671	24.913	1.00	10.95	C
ATOM	3910	CG	ARG	A	277	30.335	22.793	26.018	1.00	13.22	C
ATOM	3913	CD	ARG	A	277	31.103	21.490	26.229	1.00	13.28	C
ATOM	3916	NE	ARG	A	277	30.415	20.601	27.149	1.00	13.25	N
ATOM	3918	CZ	ARG	A	277	30.892	19.416	27.518	1.00	14.34	C
ATOM	3919	NH1	ARG	A	277	32.089	19.014	27.110	1.00	14.38	N
ATOM	3922	NH2	ARG	A	277	30.190	18.660	28.345	1.00	13.28	N
ATOM	3925	C	ARG	A	277	29.974	25.722	25.858	1.00	12.12	C
ATOM	3926	O	ARG	A	277	28.949	25.722	26.538	1.00	12.16	O
ATOM	3927	N	THR	A	278	31.023	26.469	26.175	1.00	12.13	N
ATOM	3929	CA	THR	A	278	31.049	27.295	27.359	1.00	11.62	C
ATOM	3931	CB	THR	A	278	32.461	27.918	27.485	1.00	12.51	C
ATOM	3933	OG1	THR	A	278	33.379	26.892	27.846	1.00	15.78	O
ATOM	3935	CG2	THR	A	278	32.551	28.829	28.624	1.00	17.34	C
ATOM	3939	C	THR	A	278	29.990	28.388	27.287	1.00	10.34	C
ATOM	3940	O	THR	A	278	29.372	28.715	28.294	1.00	11.22	O
ATOM	3941	N	GLU	A	279	29.775	28.943	26.101	1.00	10.24	N
ATOM	3943	CA	GLU	A	279	28.804	30.034	25.920	1.00	10.36	C
ATOM	3945	CB	GLU	A	279	29.090	30.744	24.607	1.00	13.04	C
ATOM	3948	CG	GLU	A	279	28.155	31.799	24.172	1.00	13.67	C
ATOM	3951	CD	GLU	A	279	27.827	32.923	25.148	1.00	11.41	C
ATOM	3952	OE1	GLU	A	279	28.413	33.084	26.245	1.00	12.14	O
ATOM	3953	OE2	GLU	A	279	26.928	33.691	24.766	1.00	13.94	O
ATOM	3954	C	GLU	A	279	27.387	29.439	25.978	1.00	10.50	C
ATOM	3955	O	GLU	A	279	26.477	30.093	26.462	1.00	10.16	O
ATOM	3956	N	LEU	A	280	27.198	28.205	25.499	1.00	10.73	N
ATOM	3958	CA	LEU	A	280	25.898	27.507	25.652	1.00	10.31	C
ATOM	3960	CB	LEU	A	280	25.846	26.124	24.973	1.00	12.52	C
ATOM	3963	CG	LEU	A	280	25.772	26.107	23.451	1.00	13.85	C
ATOM	3965	CD1	LEU	A	280	25.964	24.631	22.911	1.00	17.63	C
ATOM	3969	CD2	LEU	A	280	24.435	26.669	22.957	1.00	15.10	C
ATOM	3973	C	LEU	A	280	25.613	27.411	27.150	1.00	10.89	C
ATOM	3974	O	LEU	A	280	24.492	27.626	27.606	1.00	12.00	O
ATOM	3975	N	GLN	A	281	26.630	27.040	27.907	1.00	9.57	N
ATOM	3977	CA	GLN	A	281	26.479	26.931	29.322	1.00	11.52	C
ATOM	3979	CB	GLN	A	281	27.755	26.360	29.925	1.00	11.03	C
ATOM	3982	CG	GLN	A	281	28.028	24.891	29.487	1.00	12.22	C
ATOM	3985	CD	GLN	A	281	29.376	24.377	29.981	1.00	14.98	C
ATOM	3986	OE1	GLN	A	281	30.115	25.172	30.555	1.00	15.61	O
ATOM	3987	NE2	GLN	A	281	29.731	23.103	29.697	1.00	9.95	N
ATOM	3990	C	GLN	A	281	26.161	28.313	29.924	1.00	10.71	C
ATOM	3991	O	GLN	A	281	25.309	28.409	30.815	1.00	11.77	O
ATOM	3992	N	ASN	A	282	26.883	29.367	29.484	1.00	10.78	N
ATOM	3994	CA	ASN	A	282	26.722	30.715	30.090	1.00	10.24	C
ATOM	3996	CB	ASN	A	282	27.683	31.745	29.504	1.00	10.08	C
ATOM	3999	CG	ASN	A	282	29.136	31.482	29.812	1.00	13.02	C
ATOM	4000	OD1	ASN	A	282	29.471	30.830	30.809	1.00	14.49	O
ATOM	4001	ND2	ASN	A	282	30.003	32.000	28.973	1.00	12.29	N
ATOM	4004	C	ASN	A	282	25.275	31.172	29.788	1.00	11.08	C
ATOM	4005	O	ASN	A	282	24.588	31.667	30.681	1.00	12.10	O
ATOM	4006	N	ARG	A	283	24.829	30.902	28.575	1.00	9.30	N
ATOM	4008	CA	ARG	A	283	23.484	31.298	28.160	1.00	10.89	C
ATOM	4010	CB	ARG	A	283	23.305	31.055	26.697	1.00	10.96	C
ATOM	4013	CG	ARG	A	283	23.894	32.191	25.842	1.00	13.15	C

ATOM	4016	CD	ARG	A	283	23.768	31.880	24.383	1.00	11.91	C
ATOM	4019	NE	ARG	A	283	24.469	32.831	23.466	1.00	12.89	N
ATOM	4021	CZ	ARG	A	283	23.985	33.290	22.311	1.00	15.41	C
ATOM	4022	NH1	ARG	A	283	22.780	33.006	21.903	1.00	15.22	N
ATOM	4025	NH2	ARG	A	283	24.722	34.053	21.528	1.00	14.46	N
ATOM	4028	C	ARG	A	283	22.450	30.528	28.963	1.00	10.28	C
ATOM	4029	O	ARG	A	283	21.390	31.063	29.298	1.00	11.49	O
ATOM	4030	N	ALA	A	284	22.741	29.263	29.220	1.00	10.27	N
ATOM	4032	CA	ALA	A	284	21.789	28.438	29.957	1.00	10.07	C
ATOM	4034	CB	ALA	A	284	22.358	27.011	30.158	1.00	11.06	C
ATOM	4038	C	ALA	A	284	21.493	29.093	31.306	1.00	10.53	C
ATOM	4039	O	ALA	A	284	20.349	29.096	31.809	1.00	11.23	O
ATOM	4040	N	LYS	A	285	22.539	29.620	31.899	1.00	10.42	N
ATOM	4042	CA	LYS	A	285	22.446	30.158	33.238	1.00	10.99	C
ATOM	4044	CB	LYS	A	285	23.846	30.372	33.821	1.00	11.62	C
ATOM	4047	CG	LYS	A	285	24.664	29.120	34.054	1.00	12.18	C
ATOM	4050	CD	LYS	A	285	26.057	29.529	34.477	1.00	16.21	C
ATOM	4053	CE	LYS	A	285	27.062	28.492	34.451	1.00	15.01	C
ATOM	4056	NZ	LYS	A	285	28.349	29.067	35.077	1.00	17.35	C
ATOM	4060	C	LYS	A	285	21.566	31.386	33.281	1.00	11.59	N
ATOM	4061	O	LYS	A	285	21.120	31.753	34.363	1.00	12.70	O
ATOM	4062	N	VAL	A	286	21.419	32.094	32.168	1.00	10.88	N
ATOM	4064	CA	VAL	A	286	20.604	33.255	32.110	1.00	12.69	C
ATOM	4066	CB	VAL	A	286	20.719	33.961	30.788	1.00	12.21	C
ATOM	4068	CG1	VAL	A	286	19.838	35.220	30.746	1.00	15.12	C
ATOM	4072	CG2	VAL	A	286	22.221	34.402	30.612	1.00	13.05	C
ATOM	4076	C	VAL	A	286	19.153	32.850	32.362	1.00	13.03	C
ATOM	4077	O	VAL	A	286	18.399	33.651	32.960	1.00	13.04	O
ATOM	4078	N	TYR	A	287	18.788	31.649	31.885	1.00	11.44	N
ATOM	4080	CA	TYR	A	287	17.427	31.124	32.057	1.00	12.02	C
ATOM	4082	CB	TYR	A	287	16.740	30.949	30.718	1.00	12.84	C
ATOM	4085	CG	TYR	A	287	16.587	32.235	29.976	1.00	12.74	C
ATOM	4086	CD1	TYR	A	287	15.615	33.157	30.344	1.00	14.60	C
ATOM	4088	CE1	TYR	A	287	15.490	34.343	29.748	1.00	14.77	C
ATOM	4090	CZ	TYR	A	287	16.343	34.709	28.753	1.00	15.62	C
ATOM	4091	OH	TYR	A	287	16.139	35.938	28.183	1.00	18.73	O
ATOM	4093	CE2	TYR	A	287	17.372	33.852	28.377	1.00	13.12	C
ATOM	4095	CD2	TYR	A	287	17.521	32.646	28.995	1.00	11.74	C
ATOM	4097	C	TYR	A	287	17.427	29.860	32.905	1.00	12.13	C
ATOM	4098	O	TYR	A	287	17.303	28.740	32.452	1.00	13.99	O
ATOM	4099	N	ASP	A	288	17.631	30.057	34.208	1.00	12.75	N
ATOM	4101	CA	ASP	A	288	17.553	29.009	35.170	1.00	11.58	C
ATOM	4103	CB	ASP	A	288	17.721	29.636	36.551	1.00	11.65	C
ATOM	4106	CG	ASP	A	288	17.912	28.612	37.687	1.00	15.60	C
ATOM	4107	OD1	ASP	A	288	18.065	27.373	37.473	1.00	17.35	O
ATOM	4108	OD2	ASP	A	288	17.934	29.001	38.898	1.00	15.75	O
ATOM	4109	C	ASP	A	288	16.174	28.337	35.056	1.00	12.45	C
ATOM	4110	O	ASP	A	288	15.186	29.032	34.950	1.00	13.43	O
ATOM	4111	N	ILE	A	289	16.112	27.026	34.986	1.00	10.72	N
ATOM	4113	CA	ILE	A	289	14.812	26.271	34.969	1.00	12.80	C
ATOM	4115	CB	ILE	A	289	14.860	25.168	33.912	1.00	12.78	C
ATOM	4117	CG1	ILE	A	289	15.042	25.785	32.535	1.00	13.67	C
ATOM	4120	CD1	ILE	A	289	13.745	26.474	31.867	1.00	13.36	C
ATOM	4124	CG2	ILE	A	289	13.659	24.220	33.989	1.00	14.37	C
ATOM	4128	C	ILE	A	289	14.517	25.742	36.352	1.00	13.79	C
ATOM	4129	O	ILE	A	289	15.376	25.140	37.045	1.00	12.95	O
ATOM	4130	N	LYS	A	290	13.299	26.006	36.825	1.00	14.91	N
ATOM	4132	CA	LYS	A	290	12.904	25.675	38.185	1.00	16.59	C

ATOM	4134	CB	LYS	A	290	12.600	26.955	38.930	1.00	17.67	C
ATOM	4137	CG	LYS	A	290	13.878	27.786	39.143	1.00	21.86	C
ATOM	4140	CD	LYS	A	290	13.627	28.893	40.134	1.00	28.07	C
ATOM	4143	CE	LYS	A	290	13.554	30.215	39.470	1.00	34.10	C
ATOM	4146	NZ	LYS	A	290	13.272	31.317	40.512	1.00	39.60	N
ATOM	4150	C	LYS	A	290	11.648	24.807	38.235	1.00	16.71	C
ATOM	4151	O	LYS	A	290	11.200	24.444	39.330	1.00	18.64	O
ATOM	4152	N	GLY	A	291	11.119	24.507	37.071	1.00	15.39	N
ATOM	4154	CA	GLY	A	291	9.895	23.740	36.907	1.00	14.24	C
ATOM	4157	C	GLY	A	291	10.134	22.294	36.570	1.00	14.85	C
ATOM	4158	O	GLY	A	291	10.997	21.990	35.707	1.00	15.05	O
ATOM	4159	N	GLY	A	292	9.376	21.387	37.185	1.00	15.54	N
ATOM	4161	CA	GLY	A	292	9.524	19.984	36.896	1.00	14.12	C
ATOM	4164	C	GLY	A	292	10.116	19.187	38.030	1.00	15.07	C
ATOM	4165	O	GLY	A	292	10.717	19.734	38.959	1.00	15.42	O
ATOM	4166	N	ILE	A	293	9.932	17.878	37.980	1.00	14.74	N
ATOM	4168	CA	ILE	A	293	10.363	17.018	39.044	1.00	15.41	C
ATOM	4170	CB	ILE	A	293	9.881	15.599	38.776	1.00	15.32	C
ATOM	4172	CG1	ILE	A	293	8.342	15.549	38.894	1.00	18.82	C
ATOM	4175	CD1	ILE	A	293	7.731	14.260	38.471	1.00	21.20	C
ATOM	4179	CG2	ILE	A	293	10.526	14.610	39.740	1.00	15.00	C
ATOM	4183	C	ILE	A	293	11.885	17.052	39.176	1.00	16.26	C
ATOM	4184	O	ILE	A	293	12.586	16.688	38.214	1.00	14.62	O
ATOM	4185	N	GLY	A	294	12.367	17.439	40.346	1.00	14.72	N
ATOM	4187	CA	GLY	A	294	13.810	17.581	40.559	1.00	15.36	C
ATOM	4190	C	GLY	A	294	14.449	18.897	40.107	1.00	13.63	C
ATOM	4191	O	GLY	A	294	15.660	19.095	40.315	1.00	15.06	O
ATOM	4192	N	ALA	A	295	13.688	19.803	39.516	1.00	14.00	N
ATOM	4194	CA	ALA	A	295	14.220	21.064	39.058	1.00	13.92	C
ATOM	4196	CB	ALA	A	295	13.381	21.661	37.869	1.00	14.66	C
ATOM	4200	C	ALA	A	295	14.226	21.990	40.236	1.00	16.73	C
ATOM	4201	O	ALA	A	295	13.451	21.811	41.178	1.00	16.12	O
ATOM	4202	N	GLY	A	296	15.094	22.986	40.227	1.00	16.79	N
ATOM	4204	CA	GLY	A	296	15.114	23.941	41.340	1.00	18.72	C
ATOM	4207	C	GLY	A	296	16.052	25.058	41.052	1.00	17.66	C
ATOM	4208	O	GLY	A	296	16.601	25.160	39.963	1.00	16.21	O
ATOM	4209	N	THR	A	297	16.240	25.979	41.992	1.00	17.88	N
ATOM	4211	CA	THR	A	297	17.144	27.068	41.712	1.00	17.28	C
ATOM	4213	CB	THR	A	297	17.117	27.981	42.941	1.00	19.91	C
ATOM	4215	OG1	THR	A	297	15.763	28.455	43.102	1.00	19.89	O
ATOM	4217	CG2	THR	A	297	17.981	29.177	42.689	1.00	19.92	C
ATOM	4221	C	THR	A	297	18.563	26.600	41.472	1.00	17.13	C
ATOM	4222	O	THR	A	297	19.104	25.832	42.248	1.00	18.37	O
ATOM	4223	N	GLY	A	298	19.193	27.074	40.410	1.00	14.91	N
ATOM	4225	CA	GLY	A	298	20.569	26.702	40.153	1.00	15.10	C
ATOM	4228	C	GLY	A	298	20.684	25.492	39.273	1.00	14.01	C
ATOM	4229	O	GLY	A	298	19.717	25.039	38.656	1.00	12.62	O
ATOM	4230	N	ASP	A	299	21.882	24.932	39.243	1.00	13.64	N
ATOM	4232	CA	ASP	A	299	22.189	23.741	38.460	1.00	13.68	C
ATOM	4234	CB	ASP	A	299	23.689	23.623	38.447	1.00	14.28	C
ATOM	4237	CG	ASP	A	299	24.229	22.342	37.843	1.00	15.32	C
ATOM	4238	OD1	ASP	A	299	23.578	21.787	36.970	1.00	13.87	O
ATOM	4239	OD2	ASP	A	299	25.330	21.885	38.238	1.00	13.70	O
ATOM	4240	C	ASP	A	299	21.507	22.602	39.092	1.00	14.87	C
ATOM	4241	O	ASP	A	299	21.657	22.381	40.306	1.00	16.32	O
ATOM	4242	N	ASP	A	300	20.664	21.901	38.348	1.00	12.69	N
ATOM	4244	CA	ASP	A	300	19.921	20.812	38.953	1.00	12.30	C
ATOM	4246	CB	ASP	A	300	18.489	21.282	39.369	1.00	12.84	C

ATOM	4249	CG	ASP	A	300	17.615	21.597	38.192	1.00	11.72	C
ATOM	4250	OD1	ASP	A	300	17.330	20.687	37.428	1.00	13.65	O
ATOM	4251	OD2	ASP	A	300	17.079	22.691	38.018	1.00	14.33	O
ATOM	4252	C	ASP	A	300	19.928	19.603	38.011	1.00	13.91	C
ATOM	4253	O	ASP	A	300	20.278	19.699	36.822	1.00	13.63	O
ATOM	4254	N	TYR	A	301	19.514	18.462	38.539	1.00	13.49	N
ATOM	4256	CA	TYR	A	301	19.627	17.220	37.803	1.00	12.93	C
ATOM	4258	CB	TYR	A	301	19.868	16.046	38.777	1.00	11.22	C
ATOM	4261	CG	TYR	A	301	18.804	15.846	39.823	1.00	13.88	C
ATOM	4262	CD1	TYR	A	301	17.648	15.225	39.523	1.00	14.91	C
ATOM	4264	CE1	TYR	A	301	16.621	15.079	40.531	1.00	17.24	C
ATOM	4266	CZ	TYR	A	301	16.809	15.580	41.788	1.00	19.26	C
ATOM	4267	OH	TYR	A	301	15.803	15.394	42.776	1.00	20.79	O
ATOM	4269	CE2	TYR	A	301	17.977	16.242	42.081	1.00	16.95	C
ATOM	4271	CD2	TYR	A	301	18.948	16.384	41.095	1.00	13.89	C
ATOM	4273	C	TYR	A	301	18.421	16.951	36.875	1.00	11.64	C
ATOM	4274	O	TYR	A	301	18.419	15.954	36.154	1.00	11.11	O
ATOM	4275	N	ALA	A	302	17.435	17.846	36.832	1.00	11.29	N
ATOM	4277	CA	ALA	A	302	16.389	17.756	35.829	1.00	10.84	C
ATOM	4279	CB	ALA	A	302	15.006	18.227	36.391	1.00	12.99	C
ATOM	4283	C	ALA	A	302	16.684	18.574	34.581	1.00	10.79	C
ATOM	4284	O	ALA	A	302	16.424	18.146	33.444	1.00	11.72	O
ATOM	4285	N	SER	A	303	17.194	19.774	34.790	1.00	10.48	N
ATOM	4287	CA	SER	A	303	17.364	20.706	33.697	1.00	9.41	C
ATOM	4289	CB	SER	A	303	16.512	21.934	33.969	1.00	9.70	C
ATOM	4292	OG	SER	A	303	16.992	22.660	35.130	1.00	12.05	O
ATOM	4294	C	SER	A	303	18.819	21.172	33.468	1.00	10.16	C
ATOM	4295	O	SER	A	303	19.049	21.949	32.566	1.00	10.53	O
ATOM	4296	N	GLY	A	304	19.742	20.739	34.303	1.00	8.73	N
ATOM	4298	CA	GLY	A	304	21.132	21.139	34.201	1.00	10.18	C
ATOM	4301	C	GLY	A	304	21.273	22.616	34.479	1.00	10.17	C
ATOM	4302	O	GLY	A	304	20.710	23.138	35.422	1.00	10.02	O
ATOM	4303	N	PHE	A	305	22.102	23.286	33.664	1.00	11.73	N
ATOM	4305	CA	PHE	A	305	22.452	24.644	33.880	1.00	10.68	C
ATOM	4307	CB	PHE	A	305	23.661	25.048	33.036	1.00	10.84	C
ATOM	4310	CG	PHE	A	305	24.977	24.418	33.419	1.00	11.70	C
ATOM	4311	CD1	PHE	A	305	25.070	23.280	34.195	1.00	12.20	C
ATOM	4313	CE1	PHE	A	305	26.316	22.689	34.511	1.00	12.74	C
ATOM	4315	CZ	PHE	A	305	27.499	23.265	33.973	1.00	11.93	C
ATOM	4317	CE2	PHE	A	305	27.380	24.372	33.184	1.00	11.62	C
ATOM	4319	CD2	PHE	A	305	26.157	24.941	32.891	1.00	12.26	C
ATOM	4321	C	PHE	A	305	21.349	25.614	33.554	1.00	11.33	C
ATOM	4322	O	PHE	A	305	21.368	26.748	34.022	1.00	11.39	O
ATOM	4323	N	GLY	A	306	20.364	25.161	32.811	1.00	10.40	N
ATOM	4325	CA	GLY	A	306	19.276	26.018	32.414	1.00	10.88	C
ATOM	4328	C	GLY	A	306	18.926	25.834	30.963	1.00	11.20	C
ATOM	4329	O	GLY	A	306	19.208	24.812	30.318	1.00	9.40	O
ATOM	4330	N	TYR	A	307	18.291	26.863	30.443	1.00	10.29	N
ATOM	4332	CA	TYR	A	307	17.803	26.905	29.077	1.00	11.10	C
ATOM	4334	CB	TYR	A	307	16.311	27.194	29.162	1.00	10.85	C
ATOM	4337	CG	TYR	A	307	15.557	27.309	27.870	1.00	10.79	C
ATOM	4338	CD1	TYR	A	307	16.087	26.885	26.660	1.00	10.35	C
ATOM	4340	CE1	TYR	A	307	15.374	27.001	25.479	1.00	10.97	C
ATOM	4342	CZ	TYR	A	307	14.086	27.458	25.503	1.00	13.85	C
ATOM	4343	OH	TYR	A	307	13.388	27.607	24.308	1.00	13.18	O
ATOM	4345	CE2	TYR	A	307	13.531	27.912	26.705	1.00	13.38	C
ATOM	4347	CD2	TYR	A	307	14.260	27.849	27.860	1.00	11.68	C
ATOM	4349	C	TYR	A	307	18.479	27.939	28.217	1.00	12.67	C

ATOM	4350	O	TYR	A	307	18.140	29.113	28.271	1.00	13.67	O
ATOM	4351	N	PRO	A	308	19.440	27.555	27.389	1.00	11.31	N
ATOM	4352	CA	PRO	A	308	20.118	28.547	26.531	1.00	11.31	C
ATOM	4354	CB	PRO	A	308	21.315	27.780	25.971	1.00	10.82	C
ATOM	4357	CG	PRO	A	308	20.941	26.293	26.070	1.00	11.80	C
ATOM	4360	CD	PRO	A	308	19.833	26.179	27.077	1.00	12.92	C
ATOM	4363	C	PRO	A	308	19.245	29.003	25.361	1.00	11.34	C
ATOM	4364	O	PRO	A	308	18.604	28.159	24.689	1.00	10.74	O
ATOM	4365	N	ARG	A	309	19.314	30.266	25.051	1.00	12.86	N
ATOM	4367	CA	ARG	A	309	18.427	30.864	24.076	1.00	13.91	C
ATOM	4369	CB	ARG	A	309	17.252	31.527	24.844	1.00	13.02	C
ATOM	4372	CG	ARG	A	309	16.469	30.638	25.781	1.00	13.54	C
ATOM	4375	CD	ARG	A	309	15.375	31.251	26.661	1.00	14.50	C
ATOM	4378	NE	ARG	A	309	14.099	31.449	25.978	1.00	15.52	N
ATOM	4380	CZ	ARG	A	309	13.022	31.993	26.525	1.00	16.18	C
ATOM	4381	NH1	ARG	A	309	13.055	32.423	27.777	1.00	12.53	N
ATOM	4384	NH2	ARG	A	309	11.891	32.006	25.832	1.00	15.18	N
ATOM	4387	C	ARG	A	309	19.139	31.870	23.213	1.00	14.57	C
ATOM	4388	O	ARG	A	309	20.288	32.256	23.468	1.00	13.36	O
ATOM	4389	N	VAL	A	310	18.455	32.367	22.180	1.00	13.70	N
ATOM	4391	CA	VAL	A	310	19.053	33.390	21.325	1.00	15.05	C
ATOM	4393	CB	VAL	A	310	18.134	33.596	20.101	1.00	14.71	C
ATOM	4395	CG1	VAL	A	310	18.580	34.793	19.258	1.00	18.54	C
ATOM	4399	CG2	VAL	A	310	18.121	32.368	19.265	1.00	14.81	C
ATOM	4403	C	VAL	A	310	19.272	34.671	22.112	1.00	16.45	C
ATOM	4404	O	VAL	A	310	20.251	35.382	21.905	1.00	15.49	O
ATOM	4405	N	LYS	A	311	18.316	34.979	22.979	1.00	17.77	N
ATOM	4407	CA	LYS	A	311	18.415	36.106	23.940	1.00	18.52	C
ATOM	4409	CB	LYS	A	311	17.942	37.380	23.244	1.00	18.11	C
ATOM	4412	CG	LYS	A	311	16.677	37.137	22.440	1.00	23.20	C
ATOM	4415	CD	LYS	A	311	15.574	38.112	22.630	1.00	33.02	C
ATOM	4418	CE	LYS	A	311	15.667	39.252	21.732	1.00	34.63	C
ATOM	4421	NZ	LYS	A	311	14.289	39.716	21.277	1.00	36.21	N
ATOM	4425	C	LYS	A	311	17.532	35.897	25.178	1.00	17.62	C
ATOM	4426	O	LYS	A	311	16.770	34.912	25.199	1.00	16.50	O
ATOM	4427	OXT	LYS	A	311	17.534	36.644	26.172	1.00	19.57	O
ATOM	4428	CA	CA	C	312	28.232	18.547	38.069	1.00	13.89	CA
ATOM	4429	CA	CA	C	313	17.608	25.091	37.856	1.00	18.60	CA
ATOM	4430	CA	CA	C	314	27.338	14.925	29.013	0.60	10.25	CA
ATOM	4431	N	ALA	B	318	2.727	2.475	36.156	1.00	30.60	N
ATOM	4433	CA	ALA	B	318	2.319	3.152	34.902	1.00	28.10	C
ATOM	4435	CB	ALA	B	318	1.428	4.295	35.200	1.00	27.75	C
ATOM	4439	C	ALA	B	318	3.422	3.533	33.900	1.00	24.85	C
ATOM	4440	O	ALA	B	318	3.103	3.596	32.739	1.00	27.46	O
ATOM	4443	N	THR	B	319	4.625	3.965	34.273	1.00	24.93	N
ATOM	4445	CA	THR	B	319	5.658	4.224	33.231	1.00	23.26	C
ATOM	4447	CB	THR	B	319	6.154	5.690	33.296	1.00	24.03	C
ATOM	4449	OG1	THR	B	319	6.811	5.953	34.535	1.00	27.37	O
ATOM	4451	CG2	THR	B	319	4.960	6.670	33.258	1.00	27.35	C
ATOM	4455	C	THR	B	319	6.926	3.305	33.235	1.00	22.75	C
ATOM	4456	O	THR	B	319	7.820	3.498	32.406	1.00	21.26	O
ATOM	4457	N	GLU	B	320	7.027	2.401	34.205	1.00	21.07	N
ATOM	4459	CA	GLU	B	320	8.177	1.559	34.324	1.00	21.49	C
ATOM	4461	CB	GLU	B	320	9.328	2.280	35.014	1.00	21.67	C
ATOM	4464	CG	GLU	B	320	8.980	2.681	36.413	1.00	25.74	C
ATOM	4467	CD	GLU	B	320	10.174	3.130	37.222	1.00	34.05	C
ATOM	4468	OE1	GLU	B	320	10.962	3.910	36.698	1.00	36.87	O
ATOM	4469	OE2	GLU	B	320	10.295	2.711	38.394	1.00	39.11	O

ATOM	4470	C	GLU	B	320	7.818	0.308	35.082	1.00	20.20	C
ATOM	4471	O	GLU	B	320	6.914	0.330	35.945	1.00	20.85	O
ATOM	4472	N	TRP	B	321	8.526	-0.774	34.748	1.00	18.06	N
ATOM	4474	CA	TRP	B	321	8.271	-2.092	35.310	1.00	17.54	C
ATOM	4476	CB	TRP	B	321	7.595	-2.961	34.277	1.00	15.93	C
ATOM	4479	CG	TRP	B	321	6.265	-2.537	33.906	1.00	18.41	C
ATOM	4480	CD1	TRP	B	321	5.089	-3.007	34.445	1.00	16.53	C
ATOM	4482	NE1	TRP	B	321	4.017	-2.406	33.836	1.00	19.73	N
ATOM	4484	CE2	TRP	B	321	4.470	-1.523	32.886	1.00	15.64	C
ATOM	4485	CD2	TRP	B	321	5.889	-1.576	32.903	1.00	15.37	C
ATOM	4486	CE3	TRP	B	321	6.596	-0.772	31.992	1.00	14.76	C
ATOM	4488	CZ3	TRP	B	321	5.852	0.097	31.140	1.00	17.06	C
ATOM	4490	CH2	TRP	B	321	4.428	0.089	31.165	1.00	17.68	C
ATOM	4492	CZ2	TRP	B	321	3.757	-0.693	32.047	1.00	18.99	C
ATOM	4494	C	TRP	B	321	9.570	-2.716	35.728	1.00	16.82	C
ATOM	4495	O	TRP	B	321	10.068	-3.654	35.131	1.00	16.09	O
ATOM	4496	N	PRO	B	322	10.186	-2.151	36.755	1.00	18.33	N
ATOM	4497	CA	PRO	B	322	11.493	-2.628	37.202	1.00	19.01	C
ATOM	4499	CB	PRO	B	322	11.829	-1.725	38.392	1.00	19.99	C
ATOM	4502	CG	PRO	B	322	10.556	-1.019	38.744	1.00	19.55	C
ATOM	4505	CD	PRO	B	322	9.651	-1.061	37.575	1.00	19.07	C
ATOM	4508	C	PRO	B	322	11.484	-4.065	37.641	1.00	19.86	C
ATOM	4509	O	PRO	B	322	12.495	-4.748	37.546	1.00	20.25	O
ATOM	4510	N	GLU	B	323	10.334	-4.557	38.050	1.00	20.04	N
ATOM	4512	CA	GLU	B	323	10.262	-5.906	38.546	1.00	20.93	C
ATOM	4514	CB	GLU	B	323	8.960	-6.041	39.331	1.00	23.24	C
ATOM	4517	CG	GLU	B	323	7.708	-5.954	38.441	1.00	26.81	C
ATOM	4520	CD	GLU	B	323	7.184	-4.530	38.089	1.00	27.51	C
ATOM	4521	OE1	GLU	B	323	7.879	-3.511	38.275	1.00	20.70	O
ATOM	4522	OE2	GLU	B	323	5.996	-4.461	37.641	1.00	30.50	O
ATOM	4523	C	GLU	B	323	10.325	-6.934	37.407	1.00	18.55	C
ATOM	4524	O	GLU	B	323	10.521	-8.111	37.642	1.00	16.50	O
ATOM	4525	N	LEU	B	324	10.256	-6.485	36.172	1.00	16.08	N
ATOM	4527	CA	LEU	B	324	10.357	-7.398	35.050	1.00	15.61	C
ATOM	4529	CB	LEU	B	324	9.626	-6.849	33.846	1.00	15.54	C
ATOM	4532	CG	LEU	B	324	8.113	-6.779	34.039	1.00	16.64	C
ATOM	4534	CD1	LEU	B	324	7.437	-6.061	32.923	1.00	19.42	C
ATOM	4538	CD2	LEU	B	324	7.648	-8.212	34.152	1.00	19.22	C
ATOM	4542	C	LEU	B	324	11.815	-7.755	34.643	1.00	14.32	C
ATOM	4543	O	LEU	B	324	12.017	-8.619	33.836	1.00	14.01	O
ATOM	4544	N	VAL	B	325	12.792	-7.073	35.189	1.00	15.66	N
ATOM	4546	CA	VAL	B	325	14.180	-7.370	34.816	1.00	15.56	C
ATOM	4548	CB	VAL	B	325	15.184	-6.410	35.456	1.00	15.71	C
ATOM	4550	CG1	VAL	B	325	16.629	-6.860	35.094	1.00	16.62	C
ATOM	4554	CG2	VAL	B	325	14.953	-4.946	34.988	1.00	14.67	C
ATOM	4558	C	VAL	B	325	14.478	-8.817	35.197	1.00	15.70	C
ATOM	4559	O	VAL	B	325	14.181	-9.219	36.316	1.00	15.01	O
ATOM	4560	N	GLY	B	326	14.985	-9.609	34.247	1.00	16.26	N
ATOM	4562	CA	GLY	B	326	15.302	-11.008	34.494	1.00	15.67	C
ATOM	4565	C	GLY	B	326	14.166	-11.958	34.140	1.00	16.74	C
ATOM	4566	O	GLY	B	326	14.358	-13.159	34.108	1.00	16.04	O
ATOM	4567	N	LYS	B	327	12.957	-11.432	33.950	1.00	16.30	N
ATOM	4569	CA	LYS	B	327	11.848	-12.266	33.510	1.00	17.25	C
ATOM	4571	CB	LYS	B	327	10.514	-11.632	33.958	1.00	17.70	C
ATOM	4574	CG	LYS	B	327	10.573	-11.307	35.417	1.00	22.70	C
ATOM	4577	CD	LYS	B	327	9.217	-11.378	36.140	1.00	30.58	C
ATOM	4580	CE	LYS	B	327	9.404	-11.302	37.674	1.00	31.61	C
ATOM	4583	NZ	LYS	B	327	10.674	-11.962	38.027	1.00	33.63	N

ATOM	4587	C	LYS	B	327	11.837	-12.497	32.021	1.00	16.69	C
ATOM	4588	O	LYS	B	327	12.479	-11.805	31.222	1.00	15.76	O
ATOM	4589	N	SER	B	328	11.055	-13.485	31.601	1.00	18.24	N
ATOM	4591	CA	SER	B	328	10.972	-13.809	30.188	1.00	17.59	C
ATOM	4593	CB	SER	B	328	10.280	-15.154	29.994	1.00	19.45	C
ATOM	4596	OG	SER	B	328	8.887	-15.026	30.192	1.00	18.39	O
ATOM	4598	C	SER	B	328	10.206	-12.757	29.431	1.00	18.63	C
ATOM	4599	O	SER	B	328	9.375	-12.020	30.003	1.00	17.45	O
ATOM	4600	N	VAL	B	329	10.494	-12.653	28.140	1.00	18.81	N
ATOM	4602	CA	VAL	B	329	9.771	-11.690	27.299	1.00	20.52	C
ATOM	4604	CB	VAL	B	329	10.317	-11.663	25.852	1.00	21.15	C
ATOM	4606	CG1	VAL	B	329	9.817	-12.809	25.060	1.00	22.84	C
ATOM	4610	CG2	VAL	B	329	9.914	-10.411	25.159	1.00	25.35	C
ATOM	4614	C	VAL	B	329	8.276	-11.962	27.279	1.00	20.54	C
ATOM	4615	O	VAL	B	329	7.460	-11.049	27.237	1.00	19.76	O
ATOM	4616	N	GLU	B	330	7.906	-13.228	27.332	1.00	21.77	N
ATOM	4618	CA	GLU	B	330	6.504	-13.544	27.379	1.00	22.29	C
ATOM	4620	CB	GLU	B	330	6.331	-15.048	27.153	1.00	24.60	C
ATOM	4623	CG	GLU	B	330	6.850	-15.472	25.754	1.00	27.68	C
ATOM	4626	CD	GLU	B	330	8.341	-15.854	25.674	1.00	35.11	C
ATOM	4627	OE1	GLU	B	330	9.141	-15.647	26.617	1.00	28.88	O
ATOM	4628	OE2	GLU	B	330	8.722	-16.426	24.632	1.00	41.94	O
ATOM	4629	C	GLU	B	330	5.809	-13.084	28.642	1.00	22.11	C
ATOM	4630	O	GLU	B	330	4.676	-12.586	28.584	1.00	21.27	O
ATOM	4631	N	GLU	B	331	6.452	-13.239	29.790	1.00	21.03	N
ATOM	4633	CA	GLU	B	331	5.904	-12.751	31.043	1.00	21.48	C
ATOM	4635	CB	GLU	B	331	6.730	-13.205	32.262	1.00	22.76	C
ATOM	4638	CG	GLU	B	331	5.844	-13.545	33.454	1.00	31.85	C
ATOM	4641	CD	GLU	B	331	6.490	-13.408	34.816	1.00	38.17	C
ATOM	4642	OE1	GLU	B	331	7.584	-14.024	35.014	1.00	46.35	O
ATOM	4643	OE2	GLU	B	331	5.886	-12.712	35.693	1.00	37.37	O
ATOM	4644	C	GLU	B	331	5.838	-11.243	31.046	1.00	19.51	C
ATOM	4645	O	GLU	B	331	4.892	-10.668	31.537	1.00	18.89	O
ATOM	4646	N	ALA	B	332	6.882	-10.609	30.514	1.00	18.18	N
ATOM	4648	CA	ALA	B	332	6.951	-9.187	30.538	1.00	15.95	C
ATOM	4650	CB	ALA	B	332	8.254	-8.709	29.931	1.00	16.83	C
ATOM	4654	C	ALA	B	332	5.801	-8.640	29.757	1.00	15.42	C
ATOM	4655	O	ALA	B	332	5.163	-7.697	30.182	1.00	14.99	O
ATOM	4656	N	LYS	B	333	5.580	-9.189	28.589	1.00	15.39	N
ATOM	4658	CA	LYS	B	333	4.489	-8.693	27.748	1.00	17.34	C
ATOM	4660	CB	LYS	B	333	4.458	-9.450	26.441	1.00	17.67	C
ATOM	4663	CG	LYS	B	333	5.438	-9.004	25.401	1.00	21.32	C
ATOM	4666	CD	LYS	B	333	5.200	-9.807	24.128	1.00	23.42	C
ATOM	4669	CE	LYS	B	333	6.357	-9.619	23.113	1.00	28.93	C
ATOM	4672	NZ	LYS	B	333	6.005	-10.290	21.820	1.00	28.19	N
ATOM	4676	C	LYS	B	333	3.127	-8.789	28.452	1.00	17.99	C
ATOM	4677	O	LYS	B	333	2.338	-7.868	28.410	1.00	15.95	O
ATOM	4678	N	LYS	B	334	2.858	-9.904	29.125	1.00	19.30	N
ATOM	4680	CA	LYS	B	334	1.595	-10.046	29.842	1.00	19.86	C
ATOM	4682	CB	LYS	B	334	1.417	-11.432	30.481	1.00	21.24	C
ATOM	4685	CG	LYS	B	334	0.949	-12.476	29.568	1.00	28.52	C
ATOM	4688	CD	LYS	B	334	0.499	-13.819	30.317	1.00	33.48	C
ATOM	4691	CE	LYS	B	334	0.650	-15.022	29.319	1.00	37.14	C
ATOM	4694	NZ	LYS	B	334	0.870	-14.604	27.850	1.00	36.97	N
ATOM	4698	C	LYS	B	334	1.457	-8.983	30.890	1.00	18.97	C
ATOM	4699	O	LYS	B	334	0.386	-8.343	31.021	1.00	16.86	O
ATOM	4700	N	VAL	B	335	2.522	-8.754	31.658	1.00	16.84	N
ATOM	4702	CA	VAL	B	335	2.480	-7.783	32.726	1.00	16.65	C

ATOM	4704	CB	VAL	B	335	3.743	-7.823	33.591	1.00	15.76	C
ATOM	4706	CG1	VAL	B	335	3.817	-6.655	34.612	1.00	19.24	C
ATOM	4710	CG2	VAL	B	335	3.789	-9.108	34.341	1.00	17.38	C
ATOM	4714	C	VAL	B	335	2.288	-6.382	32.203	1.00	15.76	C
ATOM	4715	O	VAL	B	335	1.494	-5.615	32.763	1.00	16.18	O
ATOM	4716	N	ILE	B	336	3.033	-6.023	31.167	1.00	15.08	N
ATOM	4718	CA	ILE	B	336	2.903	-4.703	30.635	1.00	14.79	C
ATOM	4720	CB	ILE	B	336	3.967	-4.441	29.592	1.00	14.82	C
ATOM	4722	CG1	ILE	B	336	5.290	-4.318	30.367	1.00	16.31	C
ATOM	4725	CD1	ILE	B	336	6.479	-4.602	29.579	1.00	19.31	C
ATOM	4729	CG2	ILE	B	336	3.543	-3.266	28.733	1.00	16.34	C
ATOM	4733	C	ILE	B	336	1.508	-4.472	30.074	1.00	15.10	C
ATOM	4734	O	ILE	B	336	0.914	-3.437	30.347	1.00	16.57	O
ATOM	4735	N	LEU	B	337	0.956	-5.456	29.390	1.00	15.14	N
ATOM	4737	CA	LEU	B	337	-0.343	-5.235	28.769	1.00	15.94	C
ATOM	4739	CB	LEU	B	337	-0.645	-6.290	27.727	1.00	15.77	C
ATOM	4742	CG	LEU	B	337	0.121	-6.195	26.404	1.00	13.58	C
ATOM	4744	CD1	LEU	B	337	0.021	-7.498	25.632	1.00	15.44	C
ATOM	4748	CD2	LEU	B	337	-0.350	-5.049	25.553	1.00	17.85	C
ATOM	4752	C	LEU	B	337	-1.450	-5.146	29.810	1.00	17.57	C
ATOM	4753	O	LEU	B	337	-2.511	-4.531	29.544	1.00	17.36	O
ATOM	4754	N	GLN	B	338	-1.210	-5.702	30.985	1.00	18.09	N
ATOM	4756	CA	GLN	B	338	-2.195	-5.610	32.047	1.00	21.31	C
ATOM	4758	CB	GLN	B	338	-1.830	-6.557	33.205	1.00	21.97	C
ATOM	4761	CG	GLN	B	338	-1.842	-8.050	32.775	1.00	26.01	C
ATOM	4764	CD	GLN	B	338	-1.562	-9.127	33.893	1.00	29.25	C
ATOM	4765	OE1	GLN	B	338	-0.720	-8.942	34.831	1.00	34.90	O
ATOM	4766	NE2	GLN	B	338	-2.211	-10.262	33.738	1.00	29.07	N
ATOM	4769	C	GLN	B	338	-2.398	-4.143	32.469	1.00	22.67	C
ATOM	4770	O	GLN	B	338	-3.530	-3.694	32.741	1.00	22.11	O
ATOM	4771	N	ASP	B	339	-1.318	-3.366	32.465	1.00	21.30	N
ATOM	4773	CA	ASP	B	339	-1.377	-1.936	32.761	1.00	21.98	C
ATOM	4775	CB	ASP	B	339	-0.047	-1.478	33.381	1.00	22.85	C
ATOM	4778	CG	ASP	B	339	0.213	-2.106	34.710	1.00	26.72	C
ATOM	4779	OD1	ASP	B	339	-0.740	-2.105	35.518	1.00	33.25	O
ATOM	4780	OD2	ASP	B	339	1.269	-2.680	35.026	1.00	26.47	O
ATOM	4781	C	ASP	B	339	-1.644	-1.066	31.555	1.00	22.06	C
ATOM	4782	O	ASP	B	339	-2.247	0.004	31.667	1.00	23.60	O
ATOM	4783	N	LYS	B	340	-1.218	-1.515	30.387	1.00	19.19	N
ATOM	4785	CA	LYS	B	340	-1.226	-0.722	29.218	1.00	18.98	C
ATOM	4787	CB	LYS	B	340	0.186	-0.070	29.118	1.00	18.88	C
ATOM	4790	CG	LYS	B	340	0.345	0.901	28.024	1.00	18.59	C
ATOM	4793	CD	LYS	B	340	1.805	1.491	28.014	1.00	19.17	C
ATOM	4796	CE	LYS	B	340	1.999	2.462	26.848	1.00	20.90	C
ATOM	4799	NZ	LYS	B	340	1.137	3.683	27.041	1.00	23.19	N
ATOM	4803	C	LYS	B	340	-1.611	-1.550	28.035	1.00	18.75	C
ATOM	4804	O	LYS	B	340	-0.822	-1.920	27.224	1.00	18.54	O
ATOM	4805	N	PRO	B	341	-2.906	-1.822	27.892	1.00	17.67	N
ATOM	4806	CA	PRO	B	341	-3.391	-2.768	26.911	1.00	17.68	C
ATOM	4808	CB	PRO	B	341	-4.926	-2.753	27.108	1.00	18.59	C
ATOM	4811	CG	PRO	B	341	-5.155	-1.955	28.331	1.00	19.20	C
ATOM	4814	CD	PRO	B	341	-3.919	-1.347	28.825	1.00	20.06	C
ATOM	4817	C	PRO	B	341	-3.101	-2.444	25.491	1.00	15.31	C
ATOM	4818	O	PRO	B	341	-3.022	-3.289	24.614	1.00	19.02	O
ATOM	4819	N	GLU	B	342	-2.986	-1.143	25.254	1.00	17.33	N
ATOM	4821	CA	GLU	B	342	-2.745	-0.687	23.906	1.00	17.70	C
ATOM	4823	CB	GLU	B	342	-3.615	0.545	23.555	1.00	20.27	C
ATOM	4826	CG	GLU	B	342	-5.028	0.042	23.191	1.00	21.84	C

ATOM	4829	CD	GLU	B	342	-6.029	1.135	22.803	1.00	30.03	C
ATOM	4830	OE1	GLU	B	342	-5.646	2.108	22.127	1.00	34.62	O
ATOM	4831	OE2	GLU	B	342	-7.217	0.982	23.131	1.00	29.42	O
ATOM	4832	C	GLU	B	342	-1.232	-0.491	23.581	1.00	17.99	C
ATOM	4833	O	GLU	B	342	-0.912	-0.071	22.473	1.00	17.45	O
ATOM	4834	N	ALA	B	343	-0.348	-0.902	24.474	1.00	18.01	N
ATOM	4836	CA	ALA	B	343	1.075	-0.825	24.187	1.00	17.75	C
ATOM	4838	CB	ALA	B	343	1.886	-1.320	25.374	1.00	17.76	C
ATOM	4842	C	ALA	B	343	1.501	-1.509	22.934	1.00	18.41	C
ATOM	4843	O	ALA	B	343	1.018	-2.612	22.539	1.00	16.39	O
ATOM	4844	N	GLN	B	344	2.398	-0.808	22.223	1.00	16.93	N
ATOM	4846	CA	GLN	B	344	3.007	-1.326	21.061	1.00	16.94	C
ATOM	4848	CB	GLN	B	344	3.197	-0.264	19.951	1.00	18.67	C
ATOM	4851	CG	GLN	B	344	1.915	0.367	19.450	1.00	22.45	C
ATOM	4854	CD	GLN	B	344	1.041	-0.668	18.836	1.00	23.74	C
ATOM	4855	OE1	GLN	B	344	1.336	-1.176	17.737	1.00	28.25	O
ATOM	4856	NE2	GLN	B	344	0.022	-1.076	19.570	1.00	24.17	N
ATOM	4859	C	GLN	B	344	4.371	-1.804	21.578	1.00	16.61	C
ATOM	4860	O	GLN	B	344	5.276	-0.987	21.833	1.00	15.55	O
ATOM	4861	N	ILE	B	345	4.503	-3.109	21.745	1.00	14.81	N
ATOM	4863	CA	ILE	B	345	5.747	-3.697	22.338	1.00	15.57	C
ATOM	4865	CB	ILE	B	345	5.426	-4.864	23.229	1.00	14.52	C
ATOM	4867	CG1	ILE	B	345	4.420	-4.437	24.307	1.00	16.03	C
ATOM	4870	CD1	ILE	B	345	4.237	-5.385	25.452	1.00	21.70	C
ATOM	4874	CG2	ILE	B	345	6.683	-5.445	23.832	1.00	18.60	C
ATOM	4878	C	ILE	B	345	6.713	-4.108	21.261	1.00	15.60	C
ATOM	4879	O	ILE	B	345	6.317	-4.759	20.335	1.00	14.53	O
ATOM	4880	N	ILE	B	346	7.947	-3.618	21.338	1.00	15.09	N
ATOM	4882	CA	ILE	B	346	9.006	-3.853	20.373	1.00	17.65	C
ATOM	4884	CB	ILE	B	346	9.607	-2.448	19.887	1.00	18.73	C
ATOM	4886	CG1	ILE	B	346	8.486	-1.515	19.488	1.00	25.44	C
ATOM	4889	CD1	ILE	B	346	7.656	-2.110	18.400	1.00	27.09	C
ATOM	4893	CG2	ILE	B	346	10.538	-2.639	18.736	1.00	24.66	C
ATOM	4897	C	ILE	B	346	10.126	-4.549	21.136	1.00	15.44	C
ATOM	4898	O	ILE	B	346	10.515	-4.048	22.174	1.00	15.03	O
ATOM	4899	N	VAL	B	347	10.621	-5.685	20.637	1.00	15.30	N
ATOM	4901	CA	VAL	B	347	11.701	-6.425	21.310	1.00	14.26	C
ATOM	4903	CB	VAL	B	347	11.363	-7.916	21.411	1.00	13.95	C
ATOM	4905	CG1	VAL	B	347	12.550	-8.744	21.949	1.00	15.52	C
ATOM	4909	CG2	VAL	B	347	10.056	-8.103	22.171	1.00	16.01	C
ATOM	4913	C	VAL	B	347	12.980	-6.253	20.518	1.00	13.34	C
ATOM	4914	O	VAL	B	347	12.999	-6.387	19.275	1.00	13.71	O
ATOM	4915	N	LEU	B	348	14.025	-5.824	21.225	1.00	13.58	N
ATOM	4917	CA	LEU	B	348	15.334	-5.595	20.654	1.00	14.50	C
ATOM	4919	CB	LEU	B	348	15.629	-4.101	20.619	1.00	14.73	C
ATOM	4922	CG	LEU	B	348	14.624	-3.255	19.836	1.00	18.66	C
ATOM	4924	CD1	LEU	B	348	14.885	-1.758	20.172	1.00	20.34	C
ATOM	4928	CD2	LEU	B	348	14.781	-3.515	18.370	1.00	21.48	C
ATOM	4932	C	LEU	B	348	16.420	-6.246	21.500	1.00	13.69	C
ATOM	4933	O	LEU	B	348	16.298	-6.400	22.715	1.00	12.97	O
ATOM	4934	N	PRO	B	349	17.533	-6.626	20.864	1.00	13.80	N
ATOM	4935	CA	PRO	B	349	18.630	-7.173	21.635	1.00	12.71	C
ATOM	4937	CB	PRO	B	349	19.686	-7.528	20.564	1.00	14.22	C
ATOM	4940	CG	PRO	B	349	18.940	-7.614	19.288	1.00	17.12	C
ATOM	4943	CD	PRO	B	349	17.802	-6.586	19.422	1.00	13.86	C
ATOM	4946	C	PRO	B	349	19.238	-6.154	22.603	1.00	12.67	C
ATOM	4947	O	PRO	B	349	19.358	-4.987	22.270	1.00	10.43	O
ATOM	4948	N	VAL	B	350	19.679	-6.629	23.756	1.00	10.88	N

ATOM	4950	CA	VAL	B	350	20.463	-5.844	24.676	1.00	11.84	C
ATOM	4952	CB	VAL	B	350	20.967	-6.740	25.861	1.00	12.85	C
ATOM	4954	CG1	VAL	B	350	21.918	-7.822	25.385	1.00	14.03	C
ATOM	4958	CG2	VAL	B	350	21.614	-5.822	26.921	1.00	13.28	C
ATOM	4962	C	VAL	B	350	21.627	-5.189	23.892	1.00	10.88	C
ATOM	4963	O	VAL	B	350	22.262	-5.815	23.000	1.00	10.87	O
ATOM	4964	N	GLY	B	351	21.864	-3.926	24.205	1.00	11.86	N
ATOM	4966	CA	GLY	B	351	22.882	-3.099	23.581	1.00	11.51	C
ATOM	4969	C	GLY	B	351	22.512	-2.331	22.313	1.00	12.47	C
ATOM	4970	O	GLY	B	351	23.335	-1.618	21.744	1.00	10.98	O
ATOM	4971	N	THR	B	352	21.315	-2.561	21.822	1.00	11.64	N
ATOM	4973	CA	THR	B	352	20.841	-1.861	20.642	1.00	11.92	C
ATOM	4975	CB	THR	B	352	19.508	-2.419	20.225	1.00	13.71	C
ATOM	4977	OG1	THR	B	352	19.641	-3.812	19.860	1.00	10.89	O
ATOM	4979	CG2	THR	B	352	18.993	-1.703	18.981	1.00	12.02	C
ATOM	4983	C	THR	B	352	20.720	-0.383	20.920	1.00	11.24	C
ATOM	4984	O	THR	B	352	20.235	0.015	21.976	1.00	12.17	O
ATOM	4985	N	ILE	B	353	21.218	0.435	20.012	1.00	11.34	N
ATOM	4987	CA	ILE	B	353	21.125	1.893	20.166	1.00	11.58	C
ATOM	4989	CB	ILE	B	353	22.322	2.605	19.504	1.00	13.21	C
ATOM	4991	CG1	ILE	B	353	23.642	2.014	19.992	1.00	11.55	C
ATOM	4994	CD1	ILE	B	353	23.795	1.980	21.496	1.00	15.61	C
ATOM	4998	CG2	ILE	B	353	22.294	4.098	19.802	1.00	13.36	C
ATOM	5002	C	ILE	B	353	19.828	2.332	19.509	1.00	11.44	C
ATOM	5003	O	ILE	B	353	19.485	1.827	18.417	1.00	11.02	O
ATOM	5004	N	VAL	B	354	19.136	3.268	20.180	1.00	10.73	N
ATOM	5006	CA	VAL	B	354	17.785	3.663	19.740	1.00	11.42	C
ATOM	5008	CB	VAL	B	354	16.693	3.043	20.663	1.00	11.30	C
ATOM	5010	CG1	VAL	B	354	16.741	1.521	20.568	1.00	11.88	C
ATOM	5014	CG2	VAL	B	354	16.873	3.542	22.103	1.00	12.49	C
ATOM	5018	C	VAL	B	354	17.558	5.152	19.702	1.00	10.76	C
ATOM	5019	O	VAL	B	354	18.289	5.918	20.294	1.00	11.15	O
ATOM	5020	N	THR	B	355	16.607	5.599	18.894	1.00	10.94	N
ATOM	5022	CA	THR	B	355	16.207	7.001	18.884	1.00	12.16	C
ATOM	5024	CB	THR	B	355	15.004	7.267	17.939	1.00	13.72	C
ATOM	5026	OG1	THR	B	355	13.885	6.481	18.413	1.00	16.24	O
ATOM	5028	CG2	THR	B	355	15.313	6.840	16.561	1.00	14.33	C
ATOM	5032	C	THR	B	355	15.684	7.378	20.254	1.00	12.37	C
ATOM	5033	O	THR	B	355	15.263	6.554	21.050	1.00	11.43	O
ATOM	5034	N	MET	B	356	15.787	8.659	20.540	1.00	12.52	N
ATOM	5036	CA	MET	B	356	15.258	9.222	21.775	1.00	11.53	C
ATOM	5038	CB	MET	B	356	16.311	10.075	22.468	1.00	11.42	C
ATOM	5041	CG	MET	B	356	17.427	9.202	23.035	1.00	12.95	C
ATOM	5044	SD	MET	B	356	16.825	8.040	24.219	1.00	15.08	S
ATOM	5045	CE	MET	B	356	17.963	6.799	24.107	1.00	20.89	C
ATOM	5049	C	MET	B	356	13.952	9.961	21.568	1.00	13.71	C
ATOM	5050	O	MET	B	356	13.675	11.024	22.215	1.00	12.74	O
ATOM	5051	N	GLU	B	357	13.148	9.417	20.659	1.00	14.50	N
ATOM	5053	CA	GLU	B	357	11.765	9.869	20.543	1.00	14.30	C
ATOM	5055	CB	GLU	B	357	11.135	9.357	19.210	1.00	15.52	C
ATOM	5058	CG	GLU	B	357	9.674	9.735	19.153	1.00	15.25	C
ATOM	5061	CD	GLU	B	357	8.947	9.187	17.960	1.00	18.46	C
ATOM	5062	OE1	GLU	B	357	7.768	9.559	17.802	1.00	19.97	O
ATOM	5063	OE2	GLU	B	357	9.543	8.377	17.237	1.00	20.59	O
ATOM	5064	C	GLU	B	357	11.001	9.282	21.703	1.00	14.50	C
ATOM	5065	O	GLU	B	357	11.233	8.123	22.030	1.00	14.99	O
ATOM	5066	N	TYR	B	358	10.129	10.074	22.335	1.00	13.93	N
ATOM	5068	CA	TYR	B	358	9.207	9.612	23.363	1.00	14.38	C

ATOM	5070	CB	TYR	B	358	9.026	10.601	24.499	1.00	14.43	C
ATOM	5073	CG	TYR	B	358	8.057	10.136	25.563	1.00	12.84	C
ATOM	5074	CD1	TYR	B	358	8.436	9.165	26.487	1.00	14.52	C
ATOM	5076	CE1	TYR	B	358	7.559	8.706	27.463	1.00	19.65	C
ATOM	5078	CZ	TYR	B	358	6.266	9.240	27.504	1.00	19.95	C
ATOM	5079	OH	TYR	B	358	5.321	8.903	28.447	1.00	26.07	O
ATOM	5081	CE2	TYR	B	358	5.873	10.184	26.607	1.00	16.96	C
ATOM	5083	CD2	TYR	B	358	6.767	10.650	25.643	1.00	18.09	C
ATOM	5085	C	TYR	B	358	7.867	9.326	22.712	1.00	15.23	C
ATOM	5086	O	TYR	B	358	7.142	10.261	22.340	1.00	14.02	O
ATOM	5087	N	ARG	B	359	7.551	8.048	22.606	1.00	15.15	N
ATOM	5089	CA	ARG	B	359	6.294	7.557	22.003	1.00	16.88	C
ATOM	5091	CB	ARG	B	359	6.615	6.465	20.998	1.00	18.79	C
ATOM	5094	CG	ARG	B	359	6.824	6.884	19.703	1.00	22.92	C
ATOM	5097	CD	ARG	B	359	6.435	5.794	18.692	1.00	25.80	C
ATOM	5100	NE	ARG	B	359	7.237	6.083	17.556	1.00	25.82	N
ATOM	5102	CZ	ARG	B	359	7.515	5.241	16.593	1.00	26.84	C
ATOM	5103	NH1	ARG	B	359	7.000	3.996	16.593	1.00	26.53	N
ATOM	5106	NH2	ARG	B	359	8.297	5.668	15.627	1.00	28.90	N
ATOM	5109	C	ARG	B	359	5.449	6.946	23.095	1.00	17.14	C
ATOM	5110	O	ARG	B	359	5.767	5.861	23.625	1.00	15.98	O
ATOM	5111	N	ILE	B	360	4.401	7.656	23.504	1.00	16.16	N
ATOM	5113	CA	ILE	B	360	3.633	7.262	24.670	1.00	17.53	C
ATOM	5115	CB	ILE	B	360	2.575	8.354	24.998	1.00	17.66	C
ATOM	5117	CG1	ILE	B	360	1.895	8.067	26.333	1.00	24.45	C
ATOM	5120	CD1	ILE	B	360	1.711	9.278	27.140	1.00	28.72	C
ATOM	5124	CG2	ILE	B	360	1.506	8.417	23.930	1.00	18.76	C
ATOM	5128	C	ILE	B	360	2.947	5.899	24.595	1.00	16.17	C
ATOM	5129	O	ILE	B	360	2.649	5.307	25.629	1.00	19.59	O
ATOM	5130	N	ASP	B	361	2.692	5.431	23.402	1.00	19.19	N
ATOM	5132	CA	ASP	B	361	2.049	4.131	23.290	1.00	20.04	C
ATOM	5134	CB	ASP	B	361	1.070	4.141	22.156	1.00	22.33	C
ATOM	5137	CG	ASP	B	361	-0.210	4.932	22.509	1.00	27.91	C
ATOM	5138	OD1	ASP	B	361	-0.701	4.823	23.693	1.00	33.70	O
ATOM	5139	OD2	ASP	B	361	-0.734	5.711	21.687	1.00	38.62	O
ATOM	5140	C	ASP	B	361	3.025	2.996	23.111	1.00	19.38	C
ATOM	5141	O	ASP	B	361	2.580	1.872	22.958	1.00	18.79	O
ATOM	5142	N	ARG	B	362	4.342	3.291	23.099	1.00	15.34	N
ATOM	5144	CA	ARG	B	362	5.342	2.241	22.870	1.00	15.87	C
ATOM	5146	CB	ARG	B	362	6.480	2.793	21.992	1.00	13.90	C
ATOM	5149	CG	ARG	B	362	7.657	1.839	21.867	1.00	16.63	C
ATOM	5152	CD	ARG	B	362	8.570	2.234	20.721	1.00	16.00	C
ATOM	5155	NE	ARG	B	362	9.204	3.494	21.085	1.00	15.40	N
ATOM	5157	CZ	ARG	B	362	9.808	4.315	20.234	1.00	14.22	C
ATOM	5158	NH1	ARG	B	362	9.893	4.014	18.939	1.00	16.86	N
ATOM	5161	NH2	ARG	B	362	10.295	5.449	20.686	1.00	14.53	N
ATOM	5164	C	ARG	B	362	5.970	1.737	24.163	1.00	14.75	C
ATOM	5165	O	ARG	B	362	6.130	2.504	25.117	1.00	13.39	O
ATOM	5166	N	VAL	B	363	6.285	0.467	24.199	1.00	13.88	N
ATOM	5168	CA	VAL	B	363	7.159	-0.094	25.241	1.00	14.50	C
ATOM	5170	CB	VAL	B	363	6.448	-0.910	26.349	1.00	14.42	C
ATOM	5172	CG1	VAL	B	363	7.477	-1.351	27.372	1.00	17.68	C
ATOM	5176	CG2	VAL	B	363	5.401	-0.069	27.015	1.00	16.62	C
ATOM	5180	C	VAL	B	363	8.230	-0.943	24.576	1.00	14.33	C
ATOM	5181	O	VAL	B	363	7.928	-1.989	23.984	1.00	14.74	O
ATOM	5182	N	ARG	B	364	9.483	-0.510	24.651	1.00	13.57	N
ATOM	5184	CA	ARG	B	364	10.570	-1.349	24.131	1.00	13.59	C
ATOM	5186	CB	ARG	B	364	11.753	-0.458	23.713	1.00	12.88	C

ATOM	5189	CG	ARG	B	364	11.565	0.380	22.482	1.00	14.21	C
ATOM	5192	CD	ARG	B	364	12.671	1.411	22.216	1.00	18.75	C
ATOM	5195	NE	ARG	B	364	12.606	2.066	20.950	1.00	16.44	N
ATOM	5197	CZ	ARG	B	364	13.123	3.278	20.638	1.00	18.34	C
ATOM	5198	NH1	ARG	B	364	13.591	4.073	21.531	1.00	21.95	N
ATOM	5201	NH2	ARG	B	364	13.073	3.670	19.412	1.00	23.97	N
ATOM	5204	C	ARG	B	364	11.046	-2.339	25.177	1.00	14.09	C
ATOM	5205	O	ARG	B	364	11.154	-1.994	26.361	1.00	16.64	O
ATOM	5206	N	LEU	B	365	11.340	-3.548	24.735	1.00	13.84	N
ATOM	5208	CA	LEU	B	365	11.904	-4.519	25.617	1.00	12.64	C
ATOM	5210	CB	LEU	B	365	11.017	-5.737	25.667	1.00	14.17	C
ATOM	5213	CG	LEU	B	365	9.653	-5.571	26.305	1.00	14.30	C
ATOM	5215	CD1	LEU	B	365	8.907	-6.860	26.267	1.00	17.46	C
ATOM	5219	CD2	LEU	B	365	9.813	-5.054	27.714	1.00	18.97	C
ATOM	5223	C	LEU	B	365	13.235	-4.929	25.065	1.00	13.48	C
ATOM	5224	O	LEU	B	365	13.307	-5.386	23.919	1.00	13.99	O
ATOM	5225	N	PHE	B	366	14.271	-4.775	25.887	1.00	12.70	N
ATOM	5227	CA	PHE	B	366	15.619	-5.176	25.533	1.00	12.04	C
ATOM	5229	CB	PHE	B	366	16.651	-4.148	25.971	1.00	12.03	C
ATOM	5232	CG	PHE	B	366	16.476	-2.809	25.291	1.00	13.71	C
ATOM	5233	CD1	PHE	B	366	15.591	-1.889	25.820	1.00	13.42	C
ATOM	5235	CE1	PHE	B	366	15.373	-0.702	25.229	1.00	16.78	C
ATOM	5237	CZ	PHE	B	366	16.025	-0.376	24.078	1.00	16.52	C
ATOM	5239	CE2	PHE	B	366	16.899	-1.322	23.444	1.00	15.87	C
ATOM	5241	CD2	PHE	B	366	17.121	-2.554	24.083	1.00	15.60	C
ATOM	5243	C	PHE	B	366	15.875	-6.502	26.202	1.00	13.03	C
ATOM	5244	O	PHE	B	366	15.700	-6.682	27.407	1.00	13.72	O
ATOM	5245	N	VAL	B	367	16.319	-7.448	25.407	1.00	13.72	N
ATOM	5247	CA	VAL	B	367	16.457	-8.824	25.906	1.00	14.35	C
ATOM	5249	CB	VAL	B	367	15.408	-9.719	25.263	1.00	15.42	C
ATOM	5251	CG1	VAL	B	367	13.988	-9.325	25.626	1.00	17.97	C
ATOM	5255	CG2	VAL	B	367	15.608	-9.853	23.736	1.00	13.87	C
ATOM	5259	C	VAL	B	367	17.829	-9.418	25.654	1.00	14.47	C
ATOM	5260	O	VAL	B	367	18.508	-9.099	24.686	1.00	13.82	O
ATOM	5261	N	ASP	B	368	18.186	-10.385	26.500	1.00	15.21	N
ATOM	5263	CA	ASP	B	368	19.421	-11.145	26.337	1.00	14.26	C
ATOM	5265	CB	ASP	B	368	20.020	-11.526	27.668	1.00	12.83	C
ATOM	5268	CG	ASP	B	368	19.168	-12.492	28.461	1.00	13.78	C
ATOM	5269	OD1	ASP	B	368	18.383	-13.277	27.864	1.00	15.03	O
ATOM	5270	OD2	ASP	B	368	19.284	-12.487	29.687	1.00	14.11	O
ATOM	5271	C	ASP	B	368	19.197	-12.347	25.438	1.00	15.37	C
ATOM	5272	O	ASP	B	368	18.090	-12.572	24.940	1.00	13.77	O
ATOM	5273	N	LYS	B	369	20.201	-13.219	25.295	1.00	15.53	N
ATOM	5275	CA	LYS	B	369	20.096	-14.274	24.320	1.00	16.17	C
ATOM	5277	CB	LYS	B	369	21.492	-14.913	24.031	1.00	18.57	C
ATOM	5280	CG	LYS	B	369	22.335	-14.040	23.132	1.00	23.43	C
ATOM	5283	CD	LYS	B	369	21.692	-13.930	21.723	1.00	33.33	C
ATOM	5286	CE	LYS	B	369	21.825	-15.245	20.863	1.00	37.24	C
ATOM	5289	NZ	LYS	B	369	20.834	-15.304	19.703	1.00	39.15	N
ATOM	5293	C	LYS	B	369	19.120	-15.342	24.746	1.00	17.09	C
ATOM	5294	O	LYS	B	369	18.736	-16.166	23.914	1.00	16.83	O
ATOM	5295	N	LEU	B	370	18.744	-15.352	26.029	1.00	15.51	N
ATOM	5297	CA	LEU	B	370	17.739	-16.298	26.509	1.00	15.40	C
ATOM	5299	CB	LEU	B	370	18.053	-16.814	27.899	1.00	15.53	C
ATOM	5302	CG	LEU	B	370	19.358	-17.657	28.054	1.00	17.89	C
ATOM	5304	CD1	LEU	B	370	19.624	-17.980	29.490	1.00	16.28	C
ATOM	5308	CD2	LEU	B	370	19.237	-18.944	27.314	1.00	17.77	C
ATOM	5312	C	LEU	B	370	16.346	-15.711	26.481	1.00	17.02	C

ATOM	5313	O	LEU	B	370	15.426	-16.340	27.005	1.00	16.78	O
ATOM	5314	N	ASP	B	371	16.191	-14.538	25.884	1.00	15.62	N
ATOM	5316	CA	ASP	B	371	14.909	-13.828	25.822	1.00	17.82	C
ATOM	5318	CB	ASP	B	371	13.844	-14.610	25.070	1.00	16.70	C
ATOM	5321	CG	ASP	B	371	13.943	-14.455	23.561	1.00	26.05	C
ATOM	5322	OD1	ASP	B	371	14.579	-13.492	23.026	1.00	26.78	O
ATOM	5323	OD2	ASP	B	371	13.333	-15.252	22.835	1.00	35.44	O
ATOM	5324	C	ASP	B	371	14.392	-13.390	27.197	1.00	16.31	C
ATOM	5325	O	ASP	B	371	13.179	-13.251	27.432	1.00	15.98	O
ATOM	5326	N	ASN	B	372	15.334	-13.152	28.115	1.00	14.12	N
ATOM	5328	CA	ASN	B	372	15.057	-12.509	29.380	1.00	13.45	C
ATOM	5330	CB	ASN	B	372	15.846	-13.137	30.518	1.00	14.25	C
ATOM	5333	CG	ASN	B	372	15.359	-14.530	30.868	1.00	17.78	C
ATOM	5334	OD1	ASN	B	372	14.170	-14.830	30.726	1.00	15.50	O
ATOM	5335	ND2	ASN	B	372	16.280	-15.394	31.268	1.00	15.27	N
ATOM	5338	C	ASN	B	372	15.328	-11.025	29.328	1.00	13.56	C
ATOM	5339	O	ASN	B	372	16.185	-10.535	28.526	1.00	12.51	O
ATOM	5340	N	ILE	B	373	14.521	-10.271	30.078	1.00	12.00	N
ATOM	5342	CA	ILE	B	373	14.595	-8.793	30.098	1.00	12.80	C
ATOM	5344	CB	ILE	B	373	13.409	-8.177	30.868	1.00	12.48	C
ATOM	5346	CG1	ILE	B	373	12.115	-8.624	30.263	1.00	14.38	C
ATOM	5349	CD1	ILE	B	373	12.021	-8.386	28.913	1.00	13.59	C
ATOM	5353	CG2	ILE	B	373	13.467	-6.685	30.862	1.00	13.18	C
ATOM	5357	C	ILE	B	373	15.888	-8.319	30.716	1.00	12.70	C
ATOM	5358	O	ILE	B	373	16.217	-8.667	31.872	1.00	13.25	O
ATOM	5359	N	ALA	B	374	16.619	-7.490	29.940	1.00	12.49	N
ATOM	5361	CA	ALA	B	374	17.962	-7.065	30.334	1.00	11.98	C
ATOM	5363	CB	ALA	B	374	18.894	-6.974	29.099	1.00	11.19	C
ATOM	5367	C	ALA	B	374	18.005	-5.723	31.031	1.00	12.88	C
ATOM	5368	O	ALA	B	374	19.017	-5.394	31.640	1.00	13.61	O
ATOM	5369	N	GLU	B	375	16.957	-4.922	30.954	1.00	12.63	N
ATOM	5371	CA	GLU	B	375	16.927	-3.628	31.592	1.00	11.71	C
ATOM	5373	CB	GLU	B	375	17.669	-2.571	30.740	1.00	13.04	C
ATOM	5376	CG	GLU	B	375	17.020	-2.247	29.443	1.00	13.36	C
ATOM	5379	CD	GLU	B	375	17.854	-1.238	28.611	1.00	16.47	C
ATOM	5380	OE1	GLU	B	375	18.961	-1.591	28.279	1.00	19.52	O
ATOM	5381	OE2	GLU	B	375	17.355	-0.152	28.242	1.00	18.89	O
ATOM	5382	C	GLU	B	375	15.464	-3.195	31.858	1.00	12.84	C
ATOM	5383	O	GLU	B	375	14.563	-3.750	31.276	1.00	12.27	O
ATOM	5384	N	VAL	B	376	15.277	-2.235	32.747	1.00	12.90	N
ATOM	5386	CA	VAL	B	376	13.918	-1.872	33.175	1.00	13.25	C
ATOM	5388	CB	VAL	B	376	13.941	-0.719	34.173	1.00	13.63	C
ATOM	5390	CG1	VAL	B	376	12.515	-0.240	34.514	1.00	15.72	C
ATOM	5394	CG2	VAL	B	376	14.681	-1.129	35.424	1.00	19.49	C
ATOM	5398	C	VAL	B	376	13.110	-1.441	32.018	1.00	12.36	C
ATOM	5399	O	VAL	B	376	13.458	-0.494	31.358	1.00	12.35	O
ATOM	5400	N	PRO	B	377	12.016	-2.117	31.700	1.00	13.27	N
ATOM	5401	CA	PRO	B	377	11.169	-1.588	30.649	1.00	14.34	C
ATOM	5403	CB	PRO	B	377	10.141	-2.697	30.437	1.00	15.95	C
ATOM	5406	CG	PRO	B	377	10.777	-3.950	31.039	1.00	13.76	C
ATOM	5409	CD	PRO	B	377	11.585	-3.453	32.170	1.00	13.52	C
ATOM	5412	C	PRO	B	377	10.472	-0.302	31.046	1.00	14.46	C
ATOM	5413	O	PRO	B	377	10.078	-0.158	32.190	1.00	14.50	O
ATOM	5414	N	ARG	B	378	10.291	0.603	30.087	1.00	14.99	N
ATOM	5416	CA	ARG	B	378	9.687	1.912	30.298	1.00	14.79	C
ATOM	5418	CB	ARG	B	378	10.756	3.004	30.386	1.00	14.41	C
ATOM	5421	CG	ARG	B	378	11.717	2.809	31.542	1.00	16.49	C
ATOM	5424	CD	ARG	B	378	12.848	3.892	31.600	1.00	17.97	C

ATOM	5427	NE	ARG	B	378	13.805	3.569	32.642	1.00	15.14	N
ATOM	5429	CZ	ARG	B	378	13.602	3.673	33.949	1.00	19.35	C
ATOM	5430	NH1	ARG	B	378	12.452	4.173	34.445	1.00	21.30	N
ATOM	5433	NH2	ARG	B	378	14.548	3.250	34.752	1.00	20.05	N
ATOM	5436	C	ARG	B	378	8.797	2.263	29.129	1.00	14.34	C
ATOM	5437	O	ARG	B	378	8.974	1.810	28.013	1.00	14.31	O
ATOM	5438	N	VAL	B	379	7.801	3.052	29.411	1.00	13.60	N
ATOM	5440	CA	VAL	B	379	7.028	3.650	28.358	1.00	14.99	C
ATOM	5442	CB	VAL	B	379	5.847	4.399	28.967	1.00	16.05	C
ATOM	5444	CG1	VAL	B	379	5.148	5.163	27.928	1.00	17.97	C
ATOM	5448	CG2	VAL	B	379	4.863	3.410	29.606	1.00	19.07	C
ATOM	5452	C	VAL	B	379	7.899	4.629	27.551	1.00	13.40	C
ATOM	5453	O	VAL	B	379	8.683	5.397	28.127	1.00	13.64	O
ATOM	5454	N	GLY	B	380	7.742	4.666	26.241	1.00	13.02	N
ATOM	5456	CA	GLY	B	380	8.480	5.637	25.459	1.00	14.94	C
ATOM	5459	C	GLY	B	380	8.968	5.181	24.107	1.00	13.89	C
ATOM	5460	O	GLY	B	380	8.939	3.974	23.839	1.00	13.82	O
ATOM	5461	OXT	GLY	B	380	9.391	6.068	23.366	1.00	15.44	O
ATOM	5462	O	HOH	W	1	26.337	16.956	29.710	1.00	8.65	O
ATOM	5465	O	HOH	W	2	9.939	2.105	25.538	1.00	12.99	O
ATOM	5468	O	HOH	W	3	22.328	10.101	24.400	1.00	12.55	O
ATOM	5471	O	HOH	W	4	30.572	18.292	23.118	1.00	9.33	O
ATOM	5474	O	HOH	W	5	8.147	23.150	18.782	1.00	14.00	O
ATOM	5477	O	HOH	W	6	11.956	29.794	31.575	1.00	15.66	O
ATOM	5480	O	HOH	W	7	36.742	23.674	17.265	1.00	14.06	O
ATOM	5483	O	HOH	W	8	26.462	19.745	37.226	1.00	12.03	O
ATOM	5486	O	HOH	W	9	23.101	0.721	12.656	1.00	12.19	O
ATOM	5489	O	HOH	W	10	20.065	-2.650	26.156	1.00	20.32	O
ATOM	5492	O	HOH	W	11	18.435	36.223	15.049	1.00	20.55	O
ATOM	5495	O	HOH	W	12	18.961	-14.287	31.415	1.00	12.28	O
ATOM	5498	O	HOH	W	13	13.655	-3.630	28.503	1.00	11.25	O
ATOM	5501	O	HOH	W	14	6.772	28.494	24.564	1.00	16.02	O
ATOM	5504	O	HOH	W	15	25.827	-0.949	23.096	1.00	13.13	O
ATOM	5507	O	HOH	W	16	10.548	23.630	17.206	1.00	15.05	O
ATOM	5510	O	HOH	W	17	21.366	-0.008	27.896	1.00	14.00	O
ATOM	5513	O	HOH	W	18	6.571	29.390	22.100	1.00	18.38	O
ATOM	5516	O	HOH	W	19	25.418	4.779	24.010	1.00	11.22	O
ATOM	5519	O	HOH	W	20	15.446	15.813	32.417	1.00	13.39	O
ATOM	5522	O	HOH	W	21	5.625	22.360	17.718	1.00	14.91	O
ATOM	5525	O	HOH	W	22	27.953	5.617	25.060	1.00	12.69	O
ATOM	5528	O	HOH	W	23	13.200	17.441	16.128	1.00	12.98	O
ATOM	5531	O	HOH	W	24	42.359	19.143	18.719	1.00	14.71	O
ATOM	5534	O	HOH	W	25	24.537	-2.025	19.216	1.00	12.97	O
ATOM	5537	O	HOH	W	26	27.926	25.732	6.249	1.00	17.25	O
ATOM	5540	O	HOH	W	27	39.025	23.474	22.653	1.00	12.82	O
ATOM	5543	O	HOH	W	28	23.815	15.465	37.744	1.00	13.10	O
ATOM	5546	O	HOH	W	29	18.367	-9.817	33.092	1.00	17.61	O
ATOM	5549	O	HOH	W	30	20.380	12.554	15.652	1.00	10.66	O
ATOM	5552	O	HOH	W	31	18.651	1.596	26.271	1.00	14.85	O
ATOM	5555	O	HOH	W	32	35.209	6.007	10.838	1.00	15.93	O
ATOM	5558	O	HOH	W	33	18.465	24.874	35.632	1.00	11.70	O
ATOM	5561	O	HOH	W	34	20.815	27.470	36.539	1.00	14.90	O
ATOM	5564	O	HOH	W	35	20.733	10.911	9.565	1.00	14.64	O
ATOM	5567	O	HOH	W	36	4.788	27.744	28.587	1.00	16.40	O
ATOM	5570	O	HOH	W	37	8.972	17.007	35.207	1.00	15.88	O
ATOM	5573	O	HOH	W	38	33.433	11.882	27.279	1.00	15.71	O
ATOM	5576	O	HOH	W	39	11.974	0.247	27.662	1.00	14.69	O
ATOM	5579	O	HOH	W	40	11.026	22.081	14.883	1.00	14.23	O

ATOM	5582	O	HOH	W	41	26.884	-0.716	26.776	1.00	14.35	O
ATOM	5585	O	HOH	W	42	41.266	13.179	18.993	1.00	17.71	O
ATOM	5588	O	HOH	W	43	27.981	-2.861	17.044	1.00	20.05	O
ATOM	5591	O	HOH	W	44	2.212	-4.670	21.196	1.00	17.41	O
ATOM	5594	O	HOH	W	45	5.416	16.195	31.844	1.00	15.02	O
ATOM	5597	O	HOH	W	46	20.229	32.354	26.988	1.00	15.42	O
ATOM	5600	O	HOH	W	47	27.214	14.437	31.277	1.00	10.24	O
ATOM	5603	O	HOH	W	48	24.332	32.917	12.832	1.00	16.80	O
ATOM	5606	O	HOH	W	49	9.986	5.426	33.075	1.00	16.06	O
ATOM	5609	O	HOH	W	50	21.134	30.372	36.728	1.00	15.50	O
ATOM	5612	O	HOH	W	51	4.815	20.991	24.941	1.00	17.09	O
ATOM	5615	O	HOH	W	52	39.195	8.284	21.866	1.00	17.72	O
ATOM	5618	O	HOH	W	53	24.661	0.260	25.378	1.00	13.02	O
ATOM	5621	O	HOH	W	54	6.599	11.219	19.732	1.00	15.01	O
ATOM	5624	O	HOH	W	55	-1.402	-3.742	22.540	1.00	17.94	O
ATOM	5627	O	HOH	W	56	23.967	19.287	36.011	1.00	12.16	O
ATOM	5630	O	HOH	W	57	32.403	10.495	30.395	1.00	18.72	O
ATOM	5633	O	HOH	W	58	30.411	20.433	3.925	1.00	19.29	O
ATOM	5636	O	HOH	W	59	14.110	5.986	23.754	1.00	21.44	O
ATOM	5639	O	HOH	W	60	9.502	31.255	31.238	1.00	19.33	O
ATOM	5642	O	HOH	W	61	17.881	7.531	29.614	1.00	18.16	O
ATOM	5645	O	HOH	W	62	35.920	21.100	27.416	1.00	18.14	O
ATOM	5648	O	HOH	W	63	21.184	17.585	43.689	1.00	19.63	O
ATOM	5651	O	HOH	W	64	11.422	6.357	17.386	1.00	17.47	O
ATOM	5654	O	HOH	W	65	7.568	24.486	1.717	1.00	26.99	O
ATOM	5657	O	HOH	W	66	11.835	23.396	12.551	1.00	17.33	O
ATOM	5660	O	HOH	W	67	15.674	-0.267	13.102	1.00	28.14	O
ATOM	5663	O	HOH	W	68	35.246	4.205	18.695	1.00	18.92	O
ATOM	5666	O	HOH	W	69	12.071	7.219	35.891	1.00	17.95	O
ATOM	5669	O	HOH	W	70	33.151	1.122	14.747	1.00	19.80	O
ATOM	5672	O	HOH	W	71	22.406	17.015	36.075	1.00	12.42	O
ATOM	5675	O	HOH	W	72	20.744	5.444	32.336	1.00	24.35	O
ATOM	5678	O	HOH	W	73	20.988	-0.601	11.337	1.00	17.02	O
ATOM	5681	O	HOH	W	74	32.168	21.857	32.986	1.00	16.30	O
ATOM	5684	O	HOH	W	75	28.340	34.388	18.531	1.00	14.67	O
ATOM	5687	O	HOH	W	76	27.395	34.930	22.269	1.00	15.72	O
ATOM	5690	O	HOH	W	77	-2.881	1.257	27.203	1.00	24.36	O
ATOM	5693	O	HOH	W	78	1.320	22.974	26.514	1.00	16.10	O
ATOM	5696	O	HOH	W	79	20.014	2.049	4.590	1.00	18.49	O
ATOM	5699	O	HOH	W	80	20.131	-10.521	22.803	1.00	16.67	O
ATOM	5702	O	HOH	W	81	2.801	-12.938	26.738	1.00	21.33	O
ATOM	5705	O	HOH	W	82	13.524	14.422	42.122	1.00	22.70	O
ATOM	5708	O	HOH	W	83	41.288	13.787	8.384	1.00	21.34	O
ATOM	5711	O	HOH	W	84	33.383	31.044	25.382	1.00	20.83	O
ATOM	5714	O	HOH	W	85	39.402	29.928	19.487	1.00	19.25	O
ATOM	5717	O	HOH	W	86	14.181	-0.702	28.733	1.00	20.17	O
ATOM	5720	O	HOH	W	87	11.217	5.903	27.361	1.00	18.74	O
ATOM	5723	O	HOH	W	88	28.627	31.304	33.345	1.00	18.56	O
ATOM	5726	O	HOH	W	89	25.546	35.322	19.001	1.00	21.03	O
ATOM	5729	O	HOH	W	90	17.693	-0.865	33.818	1.00	23.45	O
ATOM	5732	O	HOH	W	91	16.853	2.781	26.050	1.00	20.34	O
ATOM	5735	O	HOH	W	92	34.612	21.168	14.066	1.00	15.33	O
ATOM	5738	O	HOH	W	93	19.619	19.119	0.936	1.00	29.35	O
ATOM	5741	O	HOH	W	94	20.721	21.727	42.621	1.00	20.03	O
ATOM	5744	O	HOH	W	95	17.040	19.477	42.629	1.00	20.78	O
ATOM	5747	O	HOH	W	96	20.111	-0.122	24.735	1.00	19.14	O
ATOM	5750	O	HOH	W	97	3.609	25.498	17.596	1.00	22.36	O
ATOM	5753	O	HOH	W	98	22.201	34.610	13.464	1.00	19.68	O

ATOM	5756	O	HOH	W	99	1.306	27.285	34.611	1.00	28.89	O
ATOM	5759	O	HOH	W	100	1.618	26.901	31.789	1.00	16.56	O
ATOM	5762	O	HOH	W	101	34.765	7.143	28.884	1.00	25.03	O
ATOM	5765	O	HOH	W	102	39.459	5.374	23.644	1.00	21.05	O
ATOM	5768	O	HOH	W	103	7.666	6.005	10.390	1.00	23.68	O
ATOM	5771	O	HOH	W	104	25.629	6.850	39.327	1.00	25.93	O
ATOM	5774	O	HOH	W	105	4.516	10.592	22.714	1.00	16.32	O
ATOM	5777	O	HOH	W	106	23.065	-8.147	22.078	1.00	22.91	O
ATOM	5780	O	HOH	W	107	15.215	5.229	8.027	1.00	18.64	O
ATOM	5783	O	HOH	W	108	9.120	-7.084	18.432	1.00	24.86	O
ATOM	5786	O	HOH	W	109	9.059	32.376	26.670	1.00	22.20	O
ATOM	5789	O	HOH	W	110	28.414	12.755	0.995	1.00	20.29	O
ATOM	5792	O	HOH	W	111	14.310	19.153	-3.544	1.00	25.42	O
ATOM	5795	O	HOH	W	112	18.007	-11.145	20.744	1.00	25.31	O
ATOM	5798	O	HOH	W	113	38.102	21.625	11.695	1.00	21.89	O
ATOM	5801	O	HOH	W	114	6.120	13.736	30.142	1.00	24.46	O
ATOM	5804	O	HOH	W	115	15.906	-18.386	31.627	1.00	22.15	O
ATOM	5807	O	HOH	W	116	22.389	33.907	19.142	1.00	22.92	O
ATOM	5810	O	HOH	W	117	32.200	35.724	21.334	1.00	26.32	O
ATOM	5813	O	HOH	W	118	2.190	17.510	6.678	1.00	25.22	O
ATOM	5816	O	HOH	W	119	1.118	4.704	29.359	1.00	25.72	O
ATOM	5819	O	HOH	W	120	9.611	1.556	17.312	1.00	23.94	O
ATOM	5822	O	HOH	W	121	3.629	23.370	16.136	1.00	22.93	O
ATOM	5825	O	HOH	W	122	32.907	25.232	8.564	1.00	22.34	O
ATOM	5828	O	HOH	W	123	-1.806	-9.230	29.885	1.00	26.14	O
ATOM	5831	O	HOH	W	124	32.230	21.567	30.291	1.00	23.29	O
ATOM	5834	O	HOH	W	125	37.450	14.678	29.329	1.00	25.24	O
ATOM	5837	O	HOH	W	126	15.339	36.760	18.883	1.00	20.61	O
ATOM	5840	O	HOH	W	127	10.235	7.567	31.063	1.00	21.51	O
ATOM	5843	O	HOH	W	128	24.897	37.442	19.549	1.00	24.86	O
ATOM	5846	O	HOH	W	129	17.030	-13.244	22.390	1.00	21.48	O
ATOM	5849	O	HOH	W	130	9.040	8.412	14.673	1.00	27.72	O
ATOM	5852	O	HOH	W	131	14.720	31.661	34.320	1.00	22.71	O
ATOM	5855	O	HOH	W	132	19.535	8.925	0.482	1.00	21.18	O
ATOM	5858	O	HOH	W	133	12.077	0.962	18.542	1.00	22.23	O
ATOM	5861	O	HOH	W	134	3.441	12.279	24.403	1.00	21.97	O
ATOM	5864	O	HOH	W	135	13.235	21.344	-4.722	1.00	25.46	O
ATOM	5867	O	HOH	W	136	4.989	14.655	27.582	1.00	28.75	O
ATOM	5870	O	HOH	W	137	-0.388	24.768	31.623	1.00	23.62	O
ATOM	5873	O	HOH	W	138	9.733	10.653	39.989	1.00	28.29	O
ATOM	5876	O	HOH	W	139	5.022	2.800	18.295	1.00	34.14	O
ATOM	5879	O	HOH	W	140	26.430	-3.864	19.091	1.00	26.57	O
ATOM	5882	O	HOH	W	141	33.127	12.459	35.197	1.00	24.55	O
ATOM	5885	O	HOH	W	142	4.529	14.653	24.602	1.00	27.79	O
ATOM	5888	O	HOH	W	143	34.889	3.006	29.679	1.00	26.45	O
ATOM	5891	O	HOH	W	144	26.472	27.781	5.265	1.00	24.30	O
ATOM	5894	O	HOH	W	145	9.844	1.973	10.352	1.00	30.48	O
ATOM	5897	O	HOH	W	146	23.113	35.988	15.667	1.00	24.26	O
ATOM	5900	O	HOH	W	147	3.506	18.934	26.329	1.00	23.36	O
ATOM	5903	O	HOH	W	148	41.932	12.669	10.942	1.00	26.60	O
ATOM	5906	O	HOH	W	149	40.619	12.671	22.354	1.00	26.08	O
ATOM	5909	O	HOH	W	150	33.062	38.217	15.479	1.00	37.76	O
ATOM	5912	O	HOH	W	151	3.554	31.071	10.635	1.00	26.96	O
ATOM	5915	O	HOH	W	152	14.084	8.928	41.767	1.00	28.97	O
ATOM	5918	O	HOH	W	153	29.827	1.222	9.591	1.00	30.85	O
ATOM	5921	O	HOH	W	154	23.088	-1.722	26.918	1.00	27.80	O
ATOM	5924	O	HOH	W	155	8.435	8.580	36.298	1.00	27.72	O
ATOM	5927	O	HOH	W	156	42.926	15.621	8.285	1.00	29.85	O

ATOM	5930	O	HOH	W	157	6.654	11.279	36.797	1.00	28.44	O
ATOM	5933	O	HOH	W	158	15.300	6.642	27.237	1.00	23.08	O
ATOM	5936	O	HOH	W	159	14.085	-11.817	20.799	1.00	27.86	O
ATOM	5939	O	HOH	W	160	-1.521	-6.774	36.408	1.00	31.93	O
ATOM	5942	O	HOH	W	161	15.519	1.708	31.201	1.00	27.02	O
ATOM	5945	O	HOH	W	162	0.621	-5.366	35.349	1.00	28.46	O
ATOM	5948	O	HOH	W	163	18.036	-12.751	33.648	1.00	22.09	O
ATOM	5951	O	HOH	W	164	32.843	18.669	30.344	1.00	28.48	O
ATOM	5954	O	HOH	W	165	27.765	11.874	38.295	1.00	18.10	O
ATOM	5957	O	HOH	W	166	1.781	17.606	13.084	1.00	28.85	O
ATOM	5960	O	HOH	W	167	20.211	0.158	6.249	1.00	29.98	O
ATOM	5963	O	HOH	W	168	2.759	19.112	32.488	1.00	24.07	O
ATOM	5966	O	HOH	W	169	33.968	18.793	32.524	1.00	23.54	O
ATOM	5969	O	HOH	W	170	-1.571	-13.592	26.165	1.00	34.45	O
ATOM	5972	O	HOH	W	171	39.370	28.627	17.071	1.00	26.29	O
ATOM	5975	O	HOH	W	172	17.376	32.794	35.436	1.00	23.98	O
ATOM	5978	O	HOH	W	173	9.391	6.761	35.029	1.00	21.74	O
ATOM	5981	O	HOH	W	174	16.352	11.687	43.877	1.00	31.51	O
ATOM	5984	O	HOH	W	175	36.018	4.292	25.853	1.00	21.19	O
ATOM	5987	O	HOH	W	176	24.899	-2.518	10.289	1.00	21.66	O
ATOM	5990	O	HOH	W	177	-1.286	2.934	25.647	1.00	31.88	O
ATOM	5993	O	HOH	W	178	13.449	-16.540	28.665	1.00	26.26	O
ATOM	5996	O	HOH	W	179	13.301	-0.613	16.357	1.00	27.05	O
ATOM	5999	O	HOH	W	180	24.842	17.585	44.930	1.00	26.85	O
ATOM	6002	O	HOH	W	181	5.856	18.874	39.008	1.00	29.19	O
ATOM	6005	O	HOH	W	182	-1.630	2.543	31.697	1.00	33.70	O
ATOM	6008	O	HOH	W	183	38.130	17.164	1.491	1.00	33.90	O
ATOM	6011	O	HOH	W	184	38.533	33.710	21.252	1.00	23.89	O
ATOM	6014	O	HOH	W	185	8.687	18.331	1.042	1.00	28.46	O
ATOM	6017	O	HOH	W	186	13.162	5.211	37.558	1.00	29.88	O
ATOM	6020	O	HOH	W	187	13.148	-16.170	33.001	1.00	24.01	O
ATOM	6023	O	HOH	W	188	17.877	11.059	1.344	1.00	30.31	O
ATOM	6026	O	HOH	W	189	1.036	-11.099	25.828	1.00	27.54	O
ATOM	6029	O	HOH	W	190	19.608	24.676	5.693	1.00	30.78	O
ATOM	6032	O	HOH	W	191	19.946	19.409	42.111	1.00	26.14	O
ATOM	6035	O	HOH	W	192	3.476	10.629	29.248	1.00	33.62	O
ATOM	6038	O	HOH	W	193	30.257	27.659	31.979	1.00	37.42	O
ATOM	6041	O	HOH	W	194	16.442	32.431	6.611	1.00	24.66	O
ATOM	6044	O	HOH	W	195	34.073	12.318	2.203	1.00	35.07	O
ATOM	6047	O	HOH	W	196	4.395	17.038	28.248	1.00	26.36	O
ATOM	6050	O	HOH	W	197	33.318	3.825	31.828	1.00	23.35	O
ATOM	6053	O	HOH	W	198	18.983	33.274	37.816	1.00	19.94	O
ATOM	6056	O	HOH	W	199	13.726	12.394	40.361	1.00	26.01	O
ATOM	6059	O	HOH	W	200	12.010	7.108	2.281	1.00	28.49	O
ATOM	6062	O	HOH	W	201	17.870	4.803	31.837	1.00	28.97	O
ATOM	6065	O	HOH	W	202	27.323	19.119	43.497	1.00	31.89	O
ATOM	6068	O	HOH	W	203	24.085	33.024	8.818	1.00	27.59	O
ATOM	6071	O	HOH	W	204	19.302	-7.180	37.095	1.00	25.01	O
ATOM	6074	O	HOH	W	205	34.921	3.097	15.744	1.00	35.90	O
ATOM	6077	O	HOH	W	206	22.046	36.365	19.883	1.00	33.71	O
ATOM	6080	O	HOH	W	207	4.178	27.080	39.663	1.00	28.68	O
ATOM	6083	O	HOH	W	208	21.450	25.719	2.335	1.00	29.50	O
ATOM	6086	O	HOH	W	209	7.625	37.543	22.457	1.00	27.39	O
ATOM	6089	O	HOH	W	210	27.905	0.363	30.805	1.00	27.13	O
ATOM	6092	O	HOH	W	211	29.963	26.817	34.574	1.00	28.33	O
ATOM	6095	O	HOH	W	212	37.812	29.413	15.021	1.00	35.13	O
ATOM	6098	O	HOH	W	213	31.600	5.299	33.905	1.00	30.36	O
ATOM	6101	O	HOH	W	214	0.934	2.893	30.953	1.00	26.27	O

ATOM	6104	O	HOH	W	215	15.151	-19.091	27.503	1.00	36.44	O
ATOM	6107	O	HOH	W	216	31.891	29.580	32.140	1.00	23.31	O
ATOM	6110	O	HOH	W	217	13.828	-7.788	38.638	1.00	33.17	O
ATOM	6113	O	HOH	W	218	37.026	8.221	8.178	1.00	43.15	O
ATOM	6116	O	HOH	W	219	12.026	-5.374	16.938	1.00	29.86	O
ATOM	6119	O	HOH	W	220	-1.767	-3.163	19.781	1.00	23.61	O
ATOM	6122	O	HOH	W	221	5.748	3.990	37.161	1.00	34.03	O
ATOM	6125	O	HOH	W	222	15.126	10.026	2.394	1.00	29.52	O
ATOM	6128	O	HOH	W	223	28.930	25.732	2.063	1.00	32.92	O
ATOM	6131	O	HOH	W	224	17.834	38.165	18.660	1.00	32.25	O
ATOM	6134	O	HOH	W	225	15.576	-9.633	19.956	1.00	29.35	O
ATOM	6137	O	HOH	W	226	21.532	33.500	36.344	1.00	30.91	O
ATOM	6140	O	HOH	W	227	37.166	25.308	14.969	1.00	30.80	O
ATOM	6143	O	HOH	W	228	4.201	13.978	20.632	1.00	29.14	O
ATOM	6146	O	HOH	W	229	-8.921	0.073	20.951	1.00	29.35	O
ATOM	6149	O	HOH	W	230	30.930	14.280	0.673	1.00	42.54	O
ATOM	6152	O	HOH	W	231	0.993	-10.363	23.294	1.00	35.64	O
ATOM	6155	O	HOH	W	232	19.283	-9.456	35.875	1.00	21.72	O
ATOM	6158	O	HOH	W	233	29.715	33.139	9.438	1.00	28.66	O
ATOM	6161	O	HOH	W	234	2.904	-7.322	21.953	1.00	29.37	O
ATOM	6164	O	HOH	W	235	-0.395	23.877	34.029	1.00	37.81	O
ATOM	6167	O	HOH	W	236	15.054	-3.907	38.561	1.00	26.91	O
ATOM	6170	O	HOH	W	237	25.729	34.682	11.457	1.00	29.23	O
ATOM	6173	O	HOH	W	238	9.385	33.323	24.057	1.00	36.55	O
ATOM	6176	O	HOH	W	239	24.093	-5.021	21.077	1.00	26.10	O
ATOM	6179	O	HOH	W	240	34.767	17.185	37.911	1.00	29.03	O
ATOM	6182	O	HOH	W	241	18.069	25.299	24.326	1.00	23.95	O
ATOM	6185	O	HOH	W	242	25.539	23.840	-0.133	1.00	27.32	O
ATOM	6188	O	HOH	W	243	-8.581	-0.882	24.380	1.00	32.46	O
ATOM	6191	O	HOH	W	244	37.140	34.955	20.025	1.00	39.20	O
ATOM	6194	O	HOH	W	245	25.828	-6.464	17.951	1.00	35.90	O
ATOM	6197	O	HOH	W	246	20.526	5.042	2.568	1.00	23.17	O
ATOM	6200	O	HOH	W	247	16.909	37.789	30.355	1.00	24.49	O
ATOM	6203	O	HOH	W	248	4.170	-13.753	24.179	1.00	34.75	O
ATOM	6206	O	HOH	W	249	4.757	29.554	36.890	1.00	27.07	O
ATOM	6209	O	HOH	W	250	14.985	25.383	44.611	1.00	36.67	O
ATOM	6212	O	HOH	W	251	21.002	34.942	26.743	1.00	24.40	O
ATOM	6215	O	HOH	W	252	35.187	37.614	16.171	1.00	41.70	O
ATOM	6218	O	HOH	W	253	9.429	35.849	24.299	1.00	29.47	O
ATOM	6221	O	HOH	W	254	22.360	-8.508	14.886	1.00	39.42	O
ATOM	6224	O	HOH	W	255	27.125	28.229	2.829	1.00	36.93	O
ATOM	6227	O	HOH	W	256	7.686	9.225	33.089	1.00	35.16	O
ATOM	6230	O	HOH	W	257	4.744	8.641	8.479	1.00	31.36	O
ATOM	6233	O	HOH	W	258	43.322	15.064	19.229	1.00	34.65	O
ATOM	6236	O	HOH	W	259	12.158	34.202	31.572	1.00	22.62	O
ATOM	6239	O	HOH	W	260	40.415	22.262	16.091	1.00	26.05	O
ATOM	6242	O	HOH	W	261	7.689	33.643	34.608	1.00	27.52	O
ATOM	6245	O	HOH	W	262	-2.516	-11.500	29.608	1.00	27.56	O
ATOM	6248	O	HOH	W	263	23.197	30.603	38.577	1.00	30.81	O
ATOM	6251	O	HOH	W	264	1.669	-4.135	18.399	1.00	34.72	O
ATOM	6254	O	HOH	W	265	31.682	18.313	2.510	1.00	27.38	O
ATOM	6257	O	HOH	W	266	21.515	33.588	40.094	1.00	30.03	O
ATOM	6260	O	HOH	W	267	16.458	13.271	-0.901	1.00	38.54	O
ATOM	6263	O	HOH	W	268	40.177	32.128	16.843	1.00	41.26	O
ATOM	6266	O	HOH	W	269	12.143	-2.734	15.885	1.00	27.02	O
ATOM	6269	O	HOH	W	270	27.486	-3.196	12.318	1.00	30.88	O
ATOM	6272	O	HOH	W	271	15.668	6.307	39.384	1.00	31.07	O
ATOM	6275	O	HOH	W	272	7.819	6.715	30.569	1.00	22.48	O

ATOM	6278	O	HOH	W	273	29.983	17.529	41.917	1.00	33.57	O
ATOM	6281	O	HOH	W	274	2.674	6.648	20.688	1.00	34.77	O
ATOM	6284	O	HOH	W	275	16.983	2.502	33.738	1.00	29.85	O
ATOM	6287	O	HOH	W	276	18.800	36.320	34.162	1.00	30.58	O
ATOM	6290	O	HOH	W	277	12.363	24.605	-1.596	1.00	34.55	O
ATOM	6293	O	HOH	W	278	14.702	17.110	-5.593	1.00	27.29	O
ATOM	6296	O	HOH	W	279	40.591	12.389	6.204	1.00	33.96	O
ATOM	6299	O	HOH	W	280	31.608	16.687	1.057	1.00	38.88	O
ATOM	6302	O	HOH	W	281	23.897	-11.952	20.222	1.00	34.68	O
ATOM	6305	O	HOH	W	282	11.219	39.478	21.517	1.00	33.54	O
ATOM	6308	O	HOH	W	283	2.552	16.703	24.563	1.00	35.86	O
ATOM	6311	O	HOH	W	284	27.258	9.495	42.694	1.00	30.97	O
ATOM	6314	O	HOH	W	285	5.535	8.881	16.549	1.00	28.65	O
ATOM	6317	O	HOH	W	286	2.189	24.192	36.099	1.00	31.47	O
ATOM	6320	O	HOH	W	287	19.058	-1.798	12.329	1.00	34.23	O
ATOM	6323	O	HOH	W	288	10.635	34.933	33.408	1.00	30.86	O
ATOM	6326	O	HOH	W	289	4.333	-0.576	36.893	1.00	44.65	O
ATOM	6329	O	HOH	W	290	25.069	21.389	-1.195	1.00	37.85	O
ATOM	6332	O	HOH	W	291	28.073	7.826	39.103	1.00	28.63	O
ATOM	6335	O	HOH	W	292	14.225	35.260	33.101	1.00	43.65	O
ATOM	6338	O	HOH	W	293	18.965	-2.916	15.137	1.00	38.32	O
ATOM	6341	O	HOH	W	294	40.370	19.000	13.716	1.00	33.50	O
ATOM	6344	O	HOH	W	295	6.261	32.033	33.639	1.00	30.04	O
ATOM	6347	O	HOH	W	296	13.696	37.943	17.160	1.00	36.07	O
ATOM	6350	O	HOH	W	297	2.518	21.734	35.950	1.00	40.41	O
ATOM	6353	O	HOH	W	298	31.821	26.389	38.109	1.00	33.84	O
ATOM	6356	O	HOH	W	299	-1.406	2.015	20.824	1.00	32.14	O
ATOM	6359	O	HOH	W	300	27.841	5.928	34.623	1.00	31.37	O
ATOM	6362	O	HOH	W	301	33.128	25.346	29.949	1.00	26.11	O
ATOM	6365	O	HOH	W	302	16.952	35.715	12.956	1.00	35.08	O
ATOM	6368	O	HOH	W	303	19.607	39.276	19.928	1.00	43.31	O
ATOM	6371	O	HOH	W	304	31.667	24.286	33.803	1.00	31.06	O
ATOM	6374	O	HOH	W	305	9.682	34.631	35.657	1.00	36.70	O
ATOM	6377	O	HOH	W	306	24.913	37.958	16.991	1.00	33.31	O
ATOM	6380	O	HOH	W	307	27.526	-1.443	8.577	1.00	31.08	O
ATOM	6383	O	HOH	W	308	34.923	14.237	35.665	1.00	33.29	O
ATOM	6386	O	HOH	W	309	23.480	3.819	33.037	1.00	28.70	O
ATOM	6389	O	HOH	W	310	39.917	30.468	13.351	1.00	43.99	O
ATOM	6392	O	HOH	W	311	20.005	30.742	39.713	1.00	31.34	O
ATOM	6395	O	HOH	W	312	1.762	19.900	10.728	1.00	33.53	O
ATOM	6398	O	HOH	W	313	21.282	35.887	11.600	1.00	34.66	O
ATOM	6401	O	HOH	W	314	22.512	-2.583	9.740	1.00	30.42	O
ATOM	6404	O	HOH	W	315	19.079	3.993	34.105	1.00	40.61	O
ATOM	6407	O	HOH	W	316	2.068	20.663	16.198	1.00	29.05	O
ATOM	6410	O	HOH	W	317	2.691	6.046	36.126	1.00	41.50	O
ATOM	6413	O	HOH	W	318	34.645	5.648	8.339	1.00	37.23	O
ATOM	6416	O	HOH	W	319	23.607	9.100	43.132	1.00	28.98	O
ATOM	6419	O	HOH	W	320	32.041	25.470	4.056	1.00	37.21	O
ATOM	6422	O	HOH	W	321	20.362	8.689	26.048	1.00	25.83	O
ATOM	6425	O	HOH	W	322	11.708	6.948	24.652	1.00	11.83	O
ATOM	6428	O	HOH	W	323	27.069	1.261	5.299	1.00	22.09	O
ATOM	6431	O	HOH	W	324	23.654	25.543	41.612	1.00	22.43	O
ATOM	6434	O	HOH	W	325	23.776	33.886	17.441	1.00	26.34	O
ATOM	6437	O	HOH	W	326	34.498	18.045	27.924	1.00	26.83	O
ATOM	6440	O	HOH	W	327	34.129	9.041	28.001	1.00	29.40	O
ATOM	6443	O	HOH	W	328	22.398	-4.833	18.306	1.00	31.97	O
ATOM	6446	O	HOH	W	329	32.650	36.061	13.569	1.00	32.16	O
ATOM	6449	O	HOH	W	330	18.875	6.699	27.476	1.00	31.00	O

ATOM	6452	O	HOH	W	331	43.627	18.936	5.210	1.00	33.15	O
ATOM	6455	O	HOH	W	332	13.390	23.630	-3.991	1.00	34.31	O
ATOM	6458	O	HOH	W	333	-0.102	6.438	34.964	1.00	48.55	O
ATOM	6461	O	HOH	W	334	-0.118	6.687	37.269	1.00	35.34	O
ATOM	6464	O	HOH	W	335	37.771	7.069	11.352	1.00	32.60	O
ATOM	6467	O	HOH	W	336	31.257	24.829	41.652	1.00	34.05	O
ATOM	6470	O	HOH	W	337	10.129	21.939	40.735	1.00	34.24	O
ATOM	6473	O	HOH	W	338	6.286	34.026	36.723	1.00	34.35	O
ATOM	6476	O	HOH	W	339	10.691	33.573	28.674	1.00	35.22	O
ATOM	6479	O	HOH	W	340	12.399	2.285	25.575	1.00	35.31	O
ATOM	6482	O	HOH	W	341	34.307	9.058	2.642	1.00	42.37	O
ATOM	6485	O	HOH	W	342	15.597	2.822	28.675	1.00	34.26	O
ATOM	6488	O	HOH	W	343	11.007	37.789	24.517	1.00	39.01	O
ATOM	6491	O	HOH	W	344	6.436	-13.362	22.903	1.00	41.47	O
ATOM	6494	O	HOH	W	345	19.680	17.126	45.857	1.00	37.81	O
ATOM	6497	O	HOH	W	346	10.533	36.113	27.412	1.00	34.50	O
ATOM	6500	O	HOH	W	347	41.809	19.887	16.869	1.00	37.61	O
ATOM	6503	O	HOH	W	348	21.611	15.053	-0.998	1.00	45.55	O
ATOM	6506	O	HOH	W	349	22.337	-9.031	17.861	1.00	49.31	O
ATOM	6509	O	HOH	W	350	9.303	25.984	-1.560	1.00	39.69	O
ATOM	6512	O	HOH	W	351	13.153	3.923	27.389	1.00	35.74	O
ATOM	6515	O	HOH	W	352	20.365	4.572	37.533	1.00	43.93	O
ATOM	6518	O	HOH	W	353	-2.246	27.322	10.724	1.00	42.74	O
ATOM	6521	O	HOH	W	354	9.435	33.000	4.908	1.00	38.59	O
ATOM	6524	O	HOH	W	355	15.473	17.843	44.371	1.00	40.00	O
ATOM	6527	O	HOH	W	356	13.009	31.258	32.197	1.00	21.10	O
ATOM	6530	O	HOH	W	357	36.838	8.242	3.607	1.00	35.04	O
ATOM	6533	O	HOH	W	358	30.674	-0.077	10.899	1.00	34.69	O
ATOM	6536	O	HOH	W	359	31.146	37.498	19.980	1.00	36.95	O
ATOM	6539	O	HOH	W	360	16.880	-0.664	8.461	1.00	39.07	O
ATOM	6542	O	HOH	W	361	40.707	6.845	20.023	1.00	32.40	O
ATOM	6545	O	HOH	W	362	19.502	25.524	0.606	1.00	41.49	O
ATOM	6548	O	HOH	W	363	27.574	22.139	44.653	1.00	52.17	O
ATOM	6551	O	HOH	W	364	11.308	11.015	41.537	1.00	41.08	O
ATOM	6554	O	HOH	W	365	9.385	-15.147	33.423	1.00	33.24	O
ATOM	6557	O	HOH	W	366	8.340	36.413	6.953	1.00	46.38	O
ATOM	6560	O	HOH	W	367	1.749	16.224	29.518	1.00	42.28	O
ATOM	6563	O	HOH	W	368	21.762	29.936	41.718	1.00	39.52	O
ATOM	6566	O	HOH	W	369	5.916	6.084	8.101	1.00	42.08	O
ATOM	6569	O	HOH	W	370	22.021	34.841	24.376	1.00	41.54	O
ATOM	6572	O	HOH	W	371	21.487	-18.393	21.594	1.00	38.90	O
ATOM	6575	O	HOH	W	372	39.073	5.237	9.752	1.00	40.75	O
ATOM	6578	O	HOH	W	373	23.013	-4.111	6.967	1.00	39.88	O
ATOM	6581	O	HOH	W	374	14.536	36.281	12.246	1.00	37.61	O
ATOM	6584	O	HOH	W	375	29.859	34.515	20.996	1.00	28.10	O
ATOM	6587	O	HOH	W	376	28.570	38.564	14.823	1.00	51.95	O
ATOM	6590	O	HOH	W	377	33.330	21.383	4.315	1.00	36.55	O
ATOM	6593	O	HOH	W	378	44.550	14.418	11.401	1.00	45.79	O
ATOM	6596	O	HOH	W	379	20.051	17.411	-1.528	1.00	37.86	O
ATOM	6599	O	HOH	W	380	0.588	25.706	15.094	1.00	42.46	O
ATOM	6602	O	HOH	W	381	4.339	-3.887	18.462	1.00	42.68	O
ATOM	6605	O	HOH	W	382	15.219	38.779	25.987	1.00	45.72	O
ATOM	6608	O	HOH	W	383	26.263	-1.807	0.657	1.00	35.43	O
ATOM	6611	O	HOH	W	384	43.222	8.889	13.058	1.00	39.12	O
ATOM	6614	O	HOH	W	385	3.804	15.072	37.146	1.00	35.83	O
ATOM	6617	O	HOH	W	386	13.685	22.152	44.161	1.00	46.34	O
ATOM	6620	O	HOH	W	387	39.745	6.714	14.451	1.00	43.87	O
ATOM	6623	O	HOH	W	388	4.160	10.246	14.729	1.00	40.70	O

ATOM	6626	O	HOH W 389	8.951	3.749	5.381	1.00	35.43	O
ATOM	6629	O	HOH W 390	12.861	-18.451	24.960	1.00	37.73	O
ATOM	6632	O	HOH W 391	2.829	15.459	20.671	1.00	39.80	O
ATOM	6635	O	HOH W 392	13.542	1.619	37.956	1.00	42.36	O
ATOM	6638	O	HOH W 393	16.727	31.361	39.312	1.00	38.23	O
ATOM	6641	O	HOH W 394	36.063	3.510	12.324	1.00	41.15	O
ATOM	6644	O	HOH W 395	5.800	1.387	38.322	1.00	38.68	O
ATOM	6647	O	HOH W 396	12.445	36.715	28.596	1.00	36.10	O
ATOM	6650	O	HOH W 397	2.782	12.760	27.641	1.00	47.29	O
ATOM	6653	O	HOH W 398	-1.700	-3.625	37.395	1.00	36.77	O
ATOM	6656	O	HOH W 399	41.093	10.367	21.318	1.00	46.59	O
ATOM	6659	O	HOH W 400	21.734	-5.069	9.760	1.00	48.11	O
ATOM	6662	O	HOH W 401	14.290	3.253	24.475	1.00	36.49	O
ATOM	6665	O	HOH W 402	22.729	2.974	-0.954	1.00	40.03	O
ATOM	6668	O	HOH W 403	4.597	11.469	0.380	1.00	42.88	O
ATOM	6671	O	HOH W 404	17.898	4.552	-0.927	1.00	39.85	O